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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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em_esthum2:*
em_esthum3:*
em_esthum4:*
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em_estro23: *
em_htc: *
gb_est107: *
gb_est108: *
gb_est109: *
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gb_est53:*
gb_est54:*
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em_esthum39:*
em_esthum31:*
em_esthum32:*
em_esthum32:*
em_esthum33:*
em_estp111:*
em_estp21:*
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gb_est71:

gb_est71:

gb_est73:

gb_est74:

gb_est74:

gb_est92:

gb_est92:

gb_est93:

gb_est95:

gb_est95:
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gb_est67:*
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gb_est103:*
gb_est104:*
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9b_est64:*
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gb_est51:*
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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gb_gss27:*
gb_gss29:*
gb_gss30:*
gb_gss31:*
gb_gss31:*
gb_gss32:*
gb_gss34:*
em_gss_rod6:*
em_gss_rod6:*
em_gss_rod7:*
em_gss_rod7:*
gb_gss36:*
gb_gss37:*
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em_gss_pln1:*
em_gss_pln2:*
em_gss_pro:*
em_gss_rod1:*
em_gss_rod2:*
em_gss_rod3:*
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em_gss_inv1:*
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em_gss_hum3:*
em_gss_hum4:*
em_gss_hum6:*
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gb_gss18:*
gb_gss19:*
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gb_gss4:*
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em_gss_rod5:*
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Result No.

Score

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82. 82

81.4 80.2 79.8 79.8 78.2 78.2 77.2

Canada

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Zea mays.
Zea mays
                                                                                                                             BG320800 972 bp mRNA EST 27-FEB-2001
Zm04_02c05_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings Ze
cDNA clone Zm04_02c05, mRNA sequence.
BG320800
BG320800.1 GI:13150478
EST.
Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings
                                           Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 972)
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CNS0072Q
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                                                                          Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC
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Aw731160 GA____
AL033013 Drosophil
AZ193531 SP_1023_B
BG365747 HVSME1000
AL053013 Drosophil
AF861909 963030B01
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BC58793 RHIZ2_56
AW731210 GA_E801
BF860491 963016605
AW596826 sj83b10.y
ALO66742 Drosophi1
BF866361 963067H09
BC560163 RHIZ2_71
BR357516 DG1_20_G0
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BE041016 OF16D06 O
BE804075 sr82h01.y
BE636682 rockefell
BF865160 963057E09
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|160 GA__Ea001
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MY-01-C-0
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BRY_1163
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                                                                                                                                                                                                                                                                                     GCSC--GCCCCAGAAGAGCTTGGTGGAGATGACGACGTCGGAGCGGCGCCAGCCCAGGTC
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DG1_114_B02.b2_A002 r
sequence.
BE355380
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Contact: Singh,J.A.
Eastern Cereal and Ollseed Research Centre
Agriculture and Agri-food Canada
960 Carling Avenue, Bldg. 20, Ottawa, Onta:
Tel: (613) 759-1662
Fax: (613) 759-1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site_2: Xho I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified library."

326 c 272 g 181 t 5 others
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/cultivar="CO328"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Zm04_AAFC_ECORC_cold_stressed_maize_seedlings"
/tissue_type="Leaf, crown"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
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55.1%;
                                Dark Grown 1 (DG1) Sorghum bicolor cDNA,
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l.8e-13;
hes 216;
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   CGCATCCCGGCACGCCTGCAGCAGCGCCCTTGGCCTCCTTCACGTCCAGCTGGTTGCCGAA
                                        geggteeegggegtggteeateaggegeageggtegtegteetegaegegteegetgaa
                                                                                                                                                        ggtgtggcccttgtagagccgccagccgtacatgtcggcggtgtcgaggcagttgatgcc
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                                                                                                                     GGCGCGCCCGTT--
                                                                                                                                                                                                                                           GATGACGACGTCGGAGCGGCGCCAGCCCAGGTCCCGGATGGCCCTGCCCCATGATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                 CTTCCGGGAGAGACCCTTGTCGTTGGGGCCCGGGCCG---CCCCAGAAGAGCTTGGTGGA
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Plant Sciences Building, 1
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequences
is 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector: 5-day-old dark-grown seedlings; Vect
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55.1%;
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Pred. No. 8.7e-13
0; Mismatches 22
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Best Local Similarity
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               tctggtagacgtcgatgtggtcgacgcccagcctgcgcagcgatccctcgcaggaggcga 671
                                                                                                                                                    cgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcgatgtggtgca 611
CGATGTGCTTCCGGGAGAGACCCTTGTCGTTGGGGCCCCGGGC--
                                                               AGTAGACGACGTCGACGTAGTCCATGTCGAGGCGGGGCGGAGCCGCGGAGGCCCCTCGA
                                                                                                                                   TGACCCAGTTCATGGCGCGCACCGTCTCCTCGACGGGCGTGGAGGCGTCGGGGGCGATGGC
                                                                                                                                                                                                     CGGTGATCTGCTGCGCGGACCACTCGGAGGTGCCCCAGTAGAAGGCCCCATCCCTGGTCGA 427
                                                                                                                                                                                                                                                                      274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The University of Georgia Plant Sciences Building, Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 489)
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DG1_114_B02.b1_A002
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POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                              made from poly-A RNA in the cioning vector ramous war. Clones to be sequenced were prepared by mass excision.

a 168 c 166 g 74 t
                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Dark Grown 1 (DG1)"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap: Site_1: XhOI, Site_2: ECORI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
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                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     Score 106.6; DB 1
Pred. No. 6.3e-11;
0; Mismatches 199
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Matches 236; Conserv
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gtgccggaccgccaggttgtacaggcactggtgggagaccatgcccagggagtggcggcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gctcctcggtgtggcccttgtagagccgccagccgtacatgtcggcggtgtcgaggcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACGCCCGCATCCCGGCACGCCTGCAGCAGCGCCTTGGCCTTCACGTCCAGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTGGAGATGACGACGTCGGAGCGGCCCAGCCCAGGTCCCGGATGGCCTGCCCCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW924405 562 bp
WS1_69_B07.b1_A002 F
mRNA sequence.
AW924405
                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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Plant Sciences Building, Rm.
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                        Department of Botany The University of Ge
                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Cordonnier-Pratt MM
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1 (bases 1 to 562)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor
                                                                                                                                                                                                                                                              POLYA-No
                                                                                                                                                                                                                                                                                                 18 20
                                                                                                                                                                                                                                                                                   primer: JEN REV
                                                                                                                  106
                                                                                                                                                                                                                                                                       quality sequence
                                        Conservative
                                                                                                                  a
                                                                                                              /clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5 week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

191 c 167 g 98 t
                                                                                                                                                                                                        /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                              Location/Qualifiers
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Water-stressed
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                                     Score 106.6; DB 122;
Pred. No. 6.3e-11;
0; Mismatches 194; 1
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                                                             Length
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M.,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE216453 728 bp mRNA EST 09-MAK-2001 HV_CEBb0010I14f Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA (HV_CEbb0010I14f, mRNA sequence.

BE216453
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Contact: Wing RA
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                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
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       /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
/tissue_type="seedling green
/lab_host="SOLR"
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277; Conserv
                                                                                                                                                                                                                                                                                                                              sequence.
BE356583
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DG1_126_E05.b1_A002 Dark
Sequences have been below Phred quality
                                                                                                          Contact: Cordonnier-Pratt Department of Botany
                                                                                                                                         An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 550)
                                                                                                                                                                                                                                                                 Sorghum bicolor
                                                                                                                                                                                                                                                                                                   EST.
                              Email: mmpratt@uga.edu
                                                                            The University of Georgia Plant Sciences Building,
                                                                                                                                                                                      Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                   sorghum.
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706 542 1805
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Pred. No. 1.8e-10;
0; Mismatches 208
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                                                                             2502,
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                                                                                                                                                                                                                                                                                                                                                             1 (DG1)
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                                                                             Athens,
                                                                                                                                                                                      Marsala,C.,
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for highest
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                                                                                                                                                         seedlings
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vector and a
hest quality
                                                                             30602-7271,
                                                                                                                                                                                                                                                                                                                                                             bicolor
                                                                                                                                                                                        Sudman,
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JOURNAL
COMMENT
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Best Local Sim
Matches 263;
                                                                             AUTHORS
                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                               cgagccagagcctgctggtgagcagcgggaacgcccgagccgcacgtgc
                                                                                                                                                                                                                                                                                                                                                                                         CCTGCAGCAGCGCCTTGGCCTTCACGTCCAGCTGGTTGCCGAAGGTCACCCACGAGC
                                                                                                                                                                                                                                                                                                                                                                                                          ggtccatcaggcgcagcgcgtcgtcgtcctcgacgcgtccgctgaagttcac---cgtgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acacctcgtcccacggcgcggaccggtcgatgtggtgcatctggtagacgtcgatgtggt 632
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                                                                                                                                                                                                                                                                                                                             CGTACGAGAGCTGGCTCACGCGGAGCCCGACCGGCCCAGGTTCTTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgcgccgtccgccctgggccagccacctgcccagctcctcggtgtgggcccttgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCGGAGGTGCCCCAGTAGAAGGCCCATCCCTGGTCGATGACCCAGTTCATGGCGCGCA 487
            Clarke,B.C., Hobbs,M. and Appels,R. Genes active in developing wheat er Unpublished (2000)
Contact: Bryan Clarke
Division of Plant Industry
                                                                                                                                                                                                                  AW448084
BRY_1624
AW448084
                                                                                         Spermatophyta; Magnoliophyta; Triticeae; Triticum.
1 (bases 1 to 840)
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence POLYA=No.
                                                                                                                                                                      bread wheat
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   .I.R.O.
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                                                                                                                                                                                                                                    BRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4558"
/clone_lib="bark Grown 1 (DG1)"
/clone="oran: 5-day-old dark-grown seedlings; Vector:
/note="organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 189 c 181 g 91 t
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                                                                                                                                                                                                     GI:12018745
                                                                                                                                                                                                                                    840 bp mRNA
Triticum aestivum
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                                                             wheat endosperm
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mRNA sequence 03-JAN-2001

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RESULT 8
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Best Local S
Matches 302
                           ORGANISM
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                                                                                                                                                                                                                                                                                 gtcggcggtgtcgaggcagttgatgccgcggtcccggggcgtggtccatcaggcgcagcgc
                                                                                                                                                                                    gagcagcgcggaacgcccgag 969
                                                                                                                                                                                                                      CTCCTTGACGTCGAGTTGCTTGCCGAAGGTCACCCACGCGCCGTAGGAGAGCTGGCTCAC
                                                                                                                                                                                                                                  CCGGAGCCCGACCGGCCCAG
                                                                                                                                                                                                                                                                    CCGGATCGCCTGCCCCATGATCTCCTCCGCGCGCCCCGTT-----
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                                                                                                                                                                                                                                                                                                                                                                  GC---CGCCCCAGAAGAGCTTGGTGGAGATGACGACGTCGGCGCGGCGCCAGCCCAGGTC
                                                                                                                                                                                                                                                                                                                                                                             gctcatctcgccgccgaccttggtcgccaggacggtgtcctcgcgccgtccgccctg
                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGCCTTGAGGCCCTCGACGATGTGCTTGCGGGAGAGGCCCCTTGTCGTTGGGCCCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGGCGTCGGGCAGTAGACCACGTCGACGTACTCCATGTCGAGCCGCTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302;
                                                   sequence.
BG556798
BG556798.1
EST.
                                                                                                BG556798
EM1_38_G03.
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPO Box 1600, Canberra, ACT, Tel: 61 2 6246 5054 Fax: 61 2 6246 5000
                                       sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bryanc@pi.csiro.au.
Location/Qualifiers
                                                                                              453 b
3.b1_A002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="endosperm"
266 c 250 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="P59-1G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Triticum
                                                              GI:13585796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .840
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                                                                                                Sorghum
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                                                                                                 bicolor
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                                                                                                 CDNA, mRNA
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AUTHORS
TITLE
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                             DEFINITION
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Best Local S
Matches 255
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Seq primer: JEN REV
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Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Reid,S.P., Cordonnier-Pratt,M.-M., Cor
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158 c 154 g 68 t
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bр ткма
2 Embryo 1 (EM1) Sorghum bicolor
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930 cgagccagagcctgctggtgagcagcgcggaacgcccgagccgcacgtgc
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                                                                                                                                                                                                                                                                                                                                         573 acacctcgtcccacggcgcggaccggtcgatgtggtgcatctggtagacgtcgatgtggt 632
                                                                                                                                                                                                                                                                                                                                                                                  548
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                               CCTGCAGCAGCGCCTTGGCCTTCACGTCCAGCTGGTTGCCGAAGGTCACCCACGAGC
                                                ggtccatcaggcgcagcgcgtcgtcgtcctcgacgcgctcagctcac---cgtgc
                                                                                                         agagccgccagccgtacatgtcggcggtgtcgaggcagttgatgccgcggtcccgggcgt
                                                                                                                                                                                                        CCTTGTCGTTGGGGCCCCGGGC---CGCCCCAGAAGAGCTTGGTGGAGATGCCGACGTCGG
                                                                                                                                                                                                                       cgacgcccagcctgcgcagcgatccctcgcaggaggcgatgatgtgccgccgccgacagcc
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BG464289
BG464289.1
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Sequences have been trimmed
below Phred quality 16. The
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An EST database from Sorghum:
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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ld_S.P., Cordonnier-Pratt,M.-M., Gingle,A. and
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                                                                                        GGCGTAGACCTTGGCGTTGTCGAAGAAGTTGACGCCCGCATCCCGGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
189 c 182 g 85 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germin
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573 acacctcgtcccacggcgcggaccggtcgatgtggtgcatctggtagacgtcgatgtggt 632
                                                                                                                                                                                                                                                                                                                                                                                                  513 agttcgacgagccgacgtaggagaccttgccgctggcgacgaggctgtccatggcctgcc 572
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                                                                                                                                                                                                                                                                          489 CCGTCTCCTCGATGGGCGTGGTGGCGTCGGGCGGTTGCGCGTACACCACGTCGACGTACT
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cgcgccgtccgccctggggccagcctgcccaccagctcctcggtgtgggcccttgt
                                                                                                               cgctgtcgttgacgcgctcatctcgccgccgaccttggtcgccagcacggtgtcct
                                                                                                                                                                                                 CCTTGTCGTTGGGCCCCTGGC - - - CGCCCCAGAAGAGCTTGGTGGAGATGACGACGTCGG
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100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Development of a genetically and physically anchored for barley genomics Unpublished (2000)
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Ning,R., Close,T.J., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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HVSMEF0001H06f Hordeum vulgare seedling root EST libra
(etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0001H06f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 552.
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/lab_host="TJC121" for site_1: EcoR1; Site_2:
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2:
197 c 179 g 73 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"Hordeum vulgare seedling HVcDNA0007 (etiolated and unstressed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4513"
/clone="HVSMEf0001H06f"
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547 ggcgacgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcgatgtg
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                                                                       gtgcatctggtagacgtcgatgtggtcgacgcccagcctgcgcagcgatccctcgcagga
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                                                  ATGGCAGTAGACGACGTCGACGTAGTCCATGTCGAGGCGGCGGAGCCGAGCCGCGGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
is 20
Seq primer: JEN REV
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The University of Georgia
Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                   /clone_lib="Dark &rown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: NoOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 181 c 172 g 83 t
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/db_xref="taxon:4558"
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Pred. No. 2.2e-08;
0; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGTTGACGCCCGCATCCCGGCACGCCTGCAGCAGCGCCTTGGCCTCCTTCACGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F. Initial assessment of gene diversity for the oomycete pathogen Phytophthora infestans based on expressed sequences Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE775466 629 bp mRNA EST 20-SEP-2000 MY-01-C-01 PinfestansMY Phytophthora infestans cDNA, mRNA sequence. BE775466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:
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Phytophthora infestans
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EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wageningen University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binnenhaven 9, P.O.Box 8025, 6700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Govers F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20056376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 629)
                                                                                                                                                   144
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31 317 483 412
1: Francine Govers@medew.fyto.wau.
                                               Conservative
                                                                                                                                          RNA was isolated from mycellum of P. infestens DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelial) and the successive number of the microtiter plate (e.g. MY-06-A-04)."

185 c 158 g 126 t 16 others
                                                                                                                                                                                                                                                   /dev_stage="4-week old vegetative, non-sporulating mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/note="Vector: pSPORT1; Site_1: 5al; ifferton non-sporulating mycelium in synthetic medium"
                                                                                                                                                                                                                                                                                                                                                  /strain="DDR7602, A1 mating
/db_xref="taxon:4787"
                                                                                                                                                                                                                                                                                                                                /clone_lib="PinfestansMY"
                                                                                                                                                                                                                                                                                                                                                                               /organism="Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                             9.3%;
47.5%;
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                                           Score 93; DB 140;
Pred. No. 2.4e-08;
0; Mismatches 279;
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ATGTGGTACTGTTGGTTGTACACGGGGCGGATCAGACCGAGCCGGTCGGCGATNTCG 550

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCACCACTTTGCCCCATGATGAGNTTTGACTGACCGTTGGCGTACACCTCAGCGTTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccaccagctcctcggtgtggcccttgtagagccgccagccgttacatgtcggcggtgtcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acgcgtccgctgaagttcaccgtgccgagccagagcctgctggtgagcagc 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggcagttgatgccgcggtcccgggcgtggtccatcaggcgcagcgcgtcgtcgtcctcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCCACGATATGCTTGCGGCTGTTGCCCACGTCGTTGGGGCCCAGANTTGGTGCCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE494103 596 bp mRNA EST 02-AUG-2000 WHE1277_H02_P03ZS Secale cereale anther cDNA library Secale cereale cDNA clone WHE1277_H02_P03, mRNA sequence.

BE494103 BE494103.1 GI:9660696
                                                                                                                                                                                                                                                                                                                                           Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C. The structure and function of the expressed portion of the wheat
                                                                                                                                                                                  quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                       genomes - Anther cDNA library from rye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secale cereale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 596
                                                                                                                                                                                                                                                                                   t Area, Western Regional Research Center
Buchanan Street, Albany, CA 94710, USA
: 5105595773
                                                                                                                                                                                                                                                                  5105595818
/db_xref="taxon:4550"
/clone="MHE1277_H02_P03"
/clone_lib="Secale cereale anther cDNA library"
/tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
                                                                                                                                                             r: Stratagene SK primer.
                                                                                                       /cultivar="Blanco"
                                                                                                                          ∕organism≔"Secale cereale′
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                                                                                                                                                                                                                                                                                                                                                 Pacific
                                                            JOURNAL
COMMENT
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REFERENCE

Spermatophyta; Magnoliophyta; Triticeae; Triticum.
1 (bases 1 to 675) Eukaryota; Viridiplantae; Triticum aestivum bread wheat AW447980.1

Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; Pooidea

AUTHORS TITLE

Division of Plant Industry C.S.I.R.O.

Box 1600,

Canberra,

ACT,

Australia

Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat en Unpublished (2000)
Contact: Bryan Clarke

endosperm

SOURCE KEYWORDS

ORGANISM

VERSION ACCESSION LOCUS

DEFINITION

AW447980 BRY\_1163 AW447980

BRY Triticum aestivum

cDNA clone P25-1D,

mRNA

sequence

675 ď

mRNA

GI:12018515

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RESULT 14
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                                                                                                                  935 cagageetg 943
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                                                                                                                                                                                                                                     265
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                                                                                                                                                                                                                                                         agccgccagccgtacatgtcggcggtgtcgaggccagttgatgcgcgcggtgcccqggcgtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGATAACCCGATGTACTTGACCTTCCCCTCCTCCACAAGCTTCTTGAGCTCACCAATC 491
                                                                               ATGCACCCG
                                                                                                                                                         GTGATGACGGCGACGCCGGCGTCGTCCTCGACCGGGGAGTTGTACGAGCCTGTGAGGCCC
                                                                                                                                                                                                                                   GTGTGGGGCCCGTAGACGTCGGAGGTGTCGAAGAAGGTGACGCCGCGGCGGAAGGCGTGC
                                                                                                                                                                                                                                                                                                              TGC-----ACCTGCTCCCGCGGCAGCTGCTTCAGCGCCTTGCCGAGGAGGATCTCGTTG
                                                                                                                                                                                                                                                                                                                                                 cgccgtccgccctgggccagccacctgcccaccagctcctcggtgtggcccttgtag
                                                                                                                                                                                                                                                                                                                                                                                            CGGCCGCAGATGGTGCTCTTGCCCTGGGCGTCCCGCTGGATCCCGAACTTGGTGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCCGAGGCGTGCAGGCTGGCGTCGCAGCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: XhOI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
melosis to late melosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the CDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
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Pred. No. 1.9e-06;
0; Mismatches 185;
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nes 226; Conserv
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                                                                                                       Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 486)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
                                               An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                                             EST
                                                                                                                                                                                                                           BG158402 486 bp mRNA
FM1_60_A12.bl_A003 Floral-Induced
propinguum cDNA, mRNA sequence.
BG158402 GI:12692066
                                                                                               Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                               Sorghum propinguum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
|Cultivar="Wyuna"
|/db_xref="taxon:4565"
|Clone="p25-1D"
|/clone=lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="endosperm"
237 c 207 g
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52.7%;
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Pred. No. 2.5e-06;
0; Mismatches 194;
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Search completed: June

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                                                                                        agcgcgtcgtcgtcctcgacgcgtcgctgaagttcac---cgtgccgagccagagcctg
                        ctggtgagcagcgcggaacgcccgagccgcacgtgc 979
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                                                                                                                                                                                                                 AGGTCCCGGATGGCCTGCCCCATGATCTCCTCGGCGCGCCCCGTT-----GGCG
                                                                                                                                                                                                                                                                                         CCCGGGC----CGCCCCAGAAGAGCTTGGTGGAGATGACGACGTCGGAGCGGCGCCCAGCCC
CTCACGCGGAGCCCGACCGGCCCAGGTTCTTGTAC
                                                                                                                                           TAGACCTCGGCGTTGTCGAAGAAGTTGACGCCCGCATCCCGGCACGCCTGCAGCAGCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism≃"Sorghum propinquum"
/db_xref="taxon:132711" ·
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56.3%;
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Pred. No. 3e-06;
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102
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Gapop 10.0 ,
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1728
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Copyright (c) 1993 - 2000 Compugen Ltd
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SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT;*;
/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT;*;
                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:
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                                                                                                                                                                                                                                                    DB
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    AAG39049
AAG35919
AAW23388
AAG41675
AAG41674
AAG41676
AAB79618
                                                                                                                                                                   AAW19736
AAW99386
AAB61981
                                                                                                                                                AAY52837
                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....LDEIFPAVASGGAAPEAWLQ 333
Sugar biosynthesis
S.erythraea dTDP-4
S. avermitilis ORF
Escherichia coli p
Arabidopsis thalia
Zea mays protein f
Shaker-like potass
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                                                  Description
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## ALIGNMENTS

RESULT AAW19736

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Sugar biosynthesis enzyme EryBII.

18-SEP-1997 (first entry)

AAW19736;

AAW19736 standard;

Protein; 333

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New genes involved in sugar biosynthesis and attachment - used to generate polyketide antimicrobials etc. with altered pattern of glycosylation % \left( 1\right) =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyketide; glycosylation; eryBII; L-mycarose; antimicrobial; antibiotic; antifungal; fungicide; anticancer; cytostatic; anthelmintic.
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-351066/32.
N-PSDB; AAT72684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donadio S, Katz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1996;
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RRESULT AAW99386 ID AAW99386 ID AAW99386 VXX AAW99386 VXX AAW Seconomy Seco
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Best Local
                          Cortes
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gene cluster; bacterium; enzyme; macrolide; antibiotic; erythromycin; secondary metabolite; eryBII; eryCIII; eryCIII; hybridisation; probe;
                                                                       (HMRI ) HOECHST MARION ROUSSEL.
                                                                                                                         12-JUN-1998;
25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                      Saccharopolyspora erythraea
                                                                                                                                                                                                                                                                                                                                                                                                        glycosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.erythraea dTDP-4-keto-L-6-deoxyhexose-2,3-reductase
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                                                                                                                                                                                                    21-JUL-1998;
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97FR-0009458.
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RESULT
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Best Local Similarity 100.
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the dTDP-4-keto-L-6-deoxyhexose-2,3-reductase enzyme encoded by the eryBII gene from the eryG-eryAIII gene cluster from the Gram-positive bacterium Saccharopolyspora erythraea. This gene cluster encodes enzymes involved in the production of the macrolide antibiotic erythromycin as a secondary metabolite. The erythromycin gene cluster spans approximately 53 kb and contains at least 20 open reading frames (ORF). The genes are used to produce hybrid secondary metabolites in S.erythraea, i.e. erythromycin analogues which may have improved properties or as hybridisation probes for isolating homologous genes involved in glycosylation of macrolactones in macrolide-producing strains (specifically oleandomycin-producing strains of Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences encoding
biosynthesis - useful for producing
particularly erythromycin analogues
                                                                      Glycosylation; avermectin; oleandrose; ORF8; AvrI.
            WO200109155-A1
                                        Streptomyces avermitilis
                                                                                                                                                                                                                 AAB61981 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                  14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                    avermitilis ORF8 (AvrI) polypeptide.
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                                                                                                                                                                                                                                                                                        asamtldeqalseldeifpavasggaapeawlq 333
                                                                                                                                                                                                                                                                                                                          ASAMTLDEQALSELDEIFPAVASGGAAPEAWLQ 333
                                                                                                                                                                                                                                                                                                                                                       graqvllpslrpaieayekfcrnlgedpaevglawvlsrpgiagavigprtpeqldsalk
                                                                                                                                                                                                                                                                                                                                                                       GRAQVLLPSLRPATEAYEKECRNLGEDPAEVGLAWVLSRPGTAGAVIGPRTPEQLDSALK
                                                                                                                                                                                                                                                                                                                                                                                                                 \verb|gvdhidvyqmhhidrsapwdevwqamdslvasgkvsyvgssnfagwhiaaaqenaarrhs||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 AA;
                                                                                                                                                 (first entry)
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                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1728; DB 20; 100.0%; Pred. No. 4.5e-165; tive 0; Mismatches 0;
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                                                                                     aglycone; biocatalysis; antibiotic;
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Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       performing biotransformations on macrolide compounds including avermectin or other macrolide aglycones. The sequences are also useful in vivo in a bacterial host, in vitro in combination with an actinomycete fermentation, and in vitro in combination with enzymatically active polypeptides that are not from the avermectin biosynthetic pathway to effect the synthesis of a pharmaceutically active compound, e.g. an antibiotic. Sequences AAB61973-981 represent polypeptides in the avermectin biosynthetic pathway, involved in the synthesis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methodology. The gene and the encoded polypeptides together with other enzymatically active polypeptides, are useful to perform combinatorial biocatalysis in vitro and in vivo in a host cell. They are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a 10 kb genomic DNA isolated from S. avermitilis that contains genes encoding proteins for glycosylation of avermectin aglycones. The polypeptides can be expressed by standard recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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                              AAY52837 standard;
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Matches Query Match Best Local

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Score 418; DB 20; Pred. No. 1.4e-33; 52; Mismatches 124;

Length Indels

36;

Gaps

7;

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Conservative

Sequence

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cc pyrolinic producing enzyme. The method of preparation of an isopremoid compound comprises using at least 1 DNA, a vector, cloned cells, their derived recombinant DNAs or transformed products in a culture system and extracting the isopremoid accumulated in the medium. The DNA encodes at least 1 of the following: (a) a compound for activating or catalysing the production of 1-deoxy-D-xylulose-5-phosphate from pyruvic acid and collycerylaldehyde-3-phosphate; (b) an enzyme producing farnesyl pyrolinic acid; (c) a protein which elevates the efficiency of synthesis of compounds and comprises a 3. or 4 amino acid sequence coptionally with 1 or more of the amino acids being deleted or substituted or an additional amino acid being inserted; (d) a protein which activates or catalyses the production of 2-C-methyl-D-crythreitol-composhate from 1-deoxy-D-xylulose-5-phosphate; or (e) a protein which activates a target compound or reaction and is a string end or hybrid of the DNA encoded in (a)-(e). Isopremoid compounds are useful in drugs (e.e.g. for the treatment of heart diseases, osteoporosis and hemostatis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1998;
05-AUG-1998;
15-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes the preparation of an isoprenoid compound comprising using at least 1 DNA e.g. encoding proteins which elevate the efficiency of the synthesis or DNA encoding a farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 70-72; 145pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of recombinant isoprenoid compounds useful for treatment heart diseases, osteoporosis and hemostatis, preventing cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preventing cancer and as immunopotentiators), health foods and antifouling coatings. The isopremoids also inhibit enzymatic reactions on the non-mevalonate pathway and can be used as antibacterials and herbicides. The present sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999;

12-AUG-1 13-AUG-1

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7-AUG-1999; 3-AUG-1999; 3-AUG-1999; 5-AUG-1999;

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Matches 102; Conservative
25-FEB-1999

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Pred. No. 7.3e
64; Mismatches
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                                                                                                                                            Shaker-like potassium ion channel; Kv beta 1; N-terminal A and B box;
                                                                                                                                                                          Shaker-like potassium
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                                                                                                                                                                                                                      AAW23388;
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                              23-FEB-1996;
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                                                                                                               Mammalia.
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         (OLYO)
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                                                                                                                                                                                                                                                                                                                                                                                         CLYNLAVRH-AELEVLPAAQAYGLGVFAWSPLHGGLLSGALEK--LAAGTA-----VKSA 239
                                                                                                                                                                                                                                                                                                                                  anrs--lvddtlrkvnglkpiaaelgvslaqlsiawcasnpnvssvitgatkesqivenm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVGRWLAQGGGRREDTVLATKV--GGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDV 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
         JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                    immune disease.
                                                                                                                                                                                                (first entry)
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99US-0161360.
99US-0161361.
99US-0161920.
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                                                                                                                                                                           ion
                                                                                                                                                                           channel beta-subunit core region Kv beta
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Pred. No. 8.
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                                                                                                                                            SPC: beta subunit; core
NAB; treatment; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
.2e-29;
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disease;
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This polypeptide sequence Kv beta 1 consists of the core region of a CC beta-subunit of a Shaker-like potassium ion channel (SPC). This core region can bind to a polypeptide consisting of the N-terminal A and B CC with the core of the NAB-S1 (the first transmembrane spanning domain) linking region of the Alpha-subunit of SPC. The polypeptides or the culcleic acid encoding them can be introduced into the cytoplasm of a cell to modulate the flow of potassium ions through a cytoplasmic cell membrane. Potassium ion channels regulate the action potentials, cardiac pocemaking and neurotransmitter release in excitable tissues. In CC non-excitable tissues they play important roles in hormone secretion, cell proliferation, cell volume regulation and lymphocyte differentiation. Molecules which bind to the alpha or beta-subunit polypeptides can be detected by contacting the polypeptides. With a putative core region of a beta-subunit respectively, and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide(s) derived from Shaker-like potassium ion channel alpha and beta subunits - used to alter potassium ion levels in a cell, e.g. for treating neurological disorders, tumours, metabolic disease
                                                                                                                             whether or not binding occurs. These polypeptides and the encoding nucleic acids may be useful in the treatment of a huge variety of disorders, e.g. neurological disorders, tumours, metabolic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Pages 51-52; 106pp;
Sequence
                                                                                               cardiac disease and autoimmune disease.
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329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease
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Matches 102; Query Match 290 234 177 117 128 287 stpeqlienlgaiqvlpkmtshvvneidni 316 188 60 70 11 LGRSALLTSRLWLGT-VNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEE 69 Local Similarity 4 lgksglrvsclglgtwvtfggqisdevaerlmtiayesgvnlfdtaevya----agkaev LVGRWLAQGGGRREDTVLATKV--GGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDV 127 wlkerivseegrkqqnklkdlspiae-----rlgctlpqlavawclrnegvssvllgs CLYNLAVRH-AELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGT------RTPEQLDSALKASAM--TLDEQALSELDEI 317 aeyhlfqrekvevqlpelyhkigvgamtwsplacgiisg---kygngvpessraslkcyq vfanrpdsntpmeeivramthvinggmamywgtsrwsameimeaysvarqfnmippvceq YQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQ ----AVKSAQGRAQV-LLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGP ilgsiikkkgwrrsslvittklywggkae---terglsrkhiieglkgslqrlqleyvdv Conservative 20.6%; 57; Score 356; DB 18; Pred. No. 2.1e-27; 57; Mismatches 131; Length 329; Indels 40; 176 286 187 59 233 10;

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XEXTXXX

18-OCT-2000 AAG41675;

(first entry)

Arabidopsis thaliana protein

fragment

SEQ IJ o. AAG41675 RESULT

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AAG41675 standard; Protein;

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07-SEP-1999;
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63; Mismatches 140;
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63; Mismatches
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promoter;
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                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
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CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar CC metabblism and oxidative phosphorylation (SMP) proteins given in CC AAB79243 to AAB 79633 which are involved in carbon metabblism and CC energy production. The C. glutamicum SMP gene can be used in vectors CC (II) for expression in host cells and production or modulation of CC production of fine chemicals, such as, an organic acid, a proteinogenic CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, CC antcleoside, a nucleotide, a lipid, a saturated or unsaturated fatty CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins CC (III) encoded by them are used for diagnosing the presence or activity of CC corynebacterium diphtheriae in a subject. (I), (II), (II) or Nost cells CC containing them are used to map genomes of organisms related to CC glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required CC in evolutionary studies, in determining SMP protein regions required CC metabolism of sugars, and in modulating high-energy molecule production cc in a cell (i.e. ATP, NADPH).
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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             evqsyldnrgriivdaldtaakglgispavtattwvrdrpgvtavivgartheqlshllk
                                          VLLPSL----RPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALK
                                                                                     SHQCLYNLAVRHAELEVLPAAQAYGLGVEAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQ
                                                                                                                              lwsvgywdegtpphevadtldyavrtgrvryagvrgysgwqlavthaasnhaaasarpvv
                                                                                                                                                           VYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAA--AQENAARRHSLGMV
                                                                                                                                                                                                               VGRWLAQGGGRREDTVLATKVGGE----MSERVNDSGLSARHIIASCEGSLRRLGVDHID 126
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DB; AAF71735.
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                                                                      {\tt vaqneysllerraegellpatqhlgvgffagaplgqgvltakyrseiphdsraastgrda}
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Pred. No. 1.6e-
53; Mismatches
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Corynebacterium glutamicum; metabolic pathway protein; MP proteinie chemical production; microorganism; organic acid; nucleos: nonproteinogenic amino acid; purine base; pyrimidine base; nuclipid; saturated fatty acid; unsaturated fatty acid; vite carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
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              AAW23389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (WP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the thropoduction of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids from Corynebacterium glutamicum encoding pathway proteins, useful for producing fine chemicals : microorganisms, including organic acids, nonproteinoger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                       ASAMTLDEQALSELDEI 317
                                                                                                                                evgsyldnrgriivdaldtaakglgispavtattwvrdrpgvtavivgartheqlshllk
                                                                                                                                                          VLLPSL----RPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALK
                                                                                                                                                                                                               SHOCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQ
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           protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic acids, nonproteinogenic amino acids, bases -
                                                                                                                                                                                                                                                                                                                                                                                                       53;
              329 AA
                                                                                                                                                                                                                                                                                                                                                                                                        Score 337; DB 22;
Pred. No. 1.6e-25;
3; Mismatches 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolic
                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                      184
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                                                                                                                                   Вþ
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                                                                                                                                                                                                                                                                                                                                     This polypeptide sequence KV beta 2 consists of the core region of a beta-subunit of a Shaker-like portassium ion channel (SPC). This core region can bind to a polypeptide consisting of the N-terminal A and B box (NAB) domain and the NAB-S1 (the first transmembrane spanning domain) linking region of the alpha-subunit of SPC. The polypeptides or the nucleic acid encoding them can be introduced into the cytoplasm of a cell to modulate the flow of potassium ions through a cytoplasmic cell membrane. Potassium ion channels regulate the action potentials, cardiac pacemaking and neurotransmitter release in excitable tissues. In non-excitable tissues they play important roles in hormone secretion, cell proliferation, cell volume regulation and lymphocyte differentiation. Molecules which bind to the alpha or beta-subunit polypeptides can be detected by contacting the polypeptides, with a putative NAB and NAB-S1 linking region of an alpha-subunit or with a putative core region of a beta-subunit respectively, and determining nucleic acids may be useful in the treatment of a huge variety of disorders, e.g. neurological disorders, tumours, metabolic diseases,
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide(s) derived from Shaker-like potassium ion channel alpha and beta subunits - used to alter potassium ion levels in a cell, e.g. for treating neurological disorders, tumours, metabolic disease and cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 53; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shaker-like
Kv beta 2; N
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour; auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shaker-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1996;
117
                                                                   60
                                                                                                   70
                                                                                                                                                                                                                         Local
                                                                                                                                                                    11 LGRSALLTSRLWLGT-VNESGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEE 69
                                                                                                                                    4
vfanrpdpntpmeeivramthvinggmamywgtsrwssmeimeaysvarqfnlippiceq
                              YQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQ
                                                                 vlgniikkkgwrrsslvittkifwggkae---terglsrkhiieglkaslerlqleyvdv 116
                                                                                                 LVGRWLAQGGGRREDTVLATKV---GGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDV
                                                                                                                                   lgksglrvsclglgtwvtfggqitdemaehlmtlaydnginlfdtaevya----agkaev
                                                                                                                                                                                                      Similarity 28.0
94; Conservative
                                                                                                                                                                                                                                                                                                                              disease and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal A and B box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potassium ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                         19.2%;
28.6%;
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                                                                                                                                                                                                        60;
                                                                                                                                                                                                    Score 331; DB 18;
Pred. No. 6.8e-25;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                              disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta subunit; core treatment; cardiac
                                                                                                                                                                                                                                       Length 329;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region;
disease;
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176
                                                                                                   127
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188

CLYNLAVRH-AELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAG---

Length 344;

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                                             comprising a preliminary screening for microorganisms with low or no 5S clavam production; (4) a microorganism which is capable of 5R clavam production and low or no 5S clavam production obtainable by a process as in (3); (5) clavulanic acid (CA) obtainable by the fermentation of a microorganism as in (4), and (6) CA which is free of any 5S clavam; (7) CA which is free of any clavam; 2-carboxylate. The methods and products can be used to produce organisms capable of producing increased amounts of clavams suitably e.g. CA, for use as antibiotics. The methods can also be used for the production of CA without the production of 5S
                                                                                                                                                                                        The present sequence represents the protein sequence of a gene specific for 5S clavam biosynthesis from Streptomyces clavuligerus (SC) and which is not essential for 5R clavam biosynthesis. The present invention also describes: (1) a process for improving 5R clavam production in a suitable microorganism comprising manipulation of DNA encoding as above and its inclusion in the microorganism; (2) a process for improving 5R clavam production in SC comprising disrupting or otherwise making defective DNA regions flanking cas 1; (3) a process for the identification of a microorganism suitable for high 5R clavam production
                                                                                                                                                                                                                                                                                                                                                                                                    DNA comprising defective 5S clavin biosynthesis gene(s) from Streptomyces clavam - useful for producing clavulanic acid w
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces clavuligerus; 5R clavum; cas1; ORF; open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces
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                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                            production of 5S clavam or clavam-2-carboxylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anders C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW69711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:: | |::: |:| |:|| |::|| |::|| aeyhmfqrekvevq1pe1fhk1gvgamtwsp1acgivsg---kydsg1ppysras1kgyq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                            Page 15-24;
                                 clavam-2-carboxylate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barton
   344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clavuligerus
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Best Local Similarity
            The present sequence represents a cell wall protein, designated 6 Candida albicans. The cell wall peptides and their corresponding antibodies are useful for treated their corresponding as well as for preventing or detecting infection of any yeast type. These include opportunistic and nosocomial infections. The peptides are also useful in the development of peptidomimetics an
small organic molecules with therapeutic,
                                                                                                                               New isolated hydrophobic protein antigens derived from the cell walls of Candida albicans and their corresponding antibodies, useful for detecting and treating yeast infection \,
                                                                                                                                                                                                 WPI;
                                                                                                      Disclosure; Fig 5A-C;
                                                                                                                                                                                                                                                                              19-FEB-1999;
19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell wall protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The 6C5 cell wall antigen of Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB08255;
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                                                                                                                                                                                                                                                                                                                    18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenic yeast.
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DB; AAA63930.
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                                                                                                                                                                                                                                                                             99US-0120764
99US-0120765
                                                                                                                                                                                                                                                                                                                                                                                                                                      yeast infection; pathogenesis inhibitor; 6C5 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
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                                                                                                                                                                                                                             DR,
                                                                                                      62pp; English.
                                                                                                                                                                                                                           Masouka
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research
               and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                    ::: | : | : | : | : | : | : | : | 336
                                   276 VLSRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEIFPA 320
                                                                                                                                  174 assmktwefvelqnvakangwhqfismqshysllyredereindyckkngiglipwspng 233
                                                                    234 ggvlcrpfdsektkqfldnkqwsslfglenvrdadkiivdrveelsvkynasmmqvslaw 293
                                                                                                      220 GGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPA----IEAYEKFCRNLGEDPAEVGLAW 275
                                                                                                                                                         1 MTTDAATHV-RLGRSALLTSRLWLGTV-----NFSGRVEDDDALRLMDHARDRGINCL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
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Search completed: June 22, 2001, 09:24:33 Job time: 109 sec

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Perfect score:
Sequence:
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US-08-907-674-1
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sequence z, Appıı	ى د	Sequence 5, Appli	Sequence 5, Appli		Sequence 20, Appl		Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 27, Appl	Sequence 3, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 5, Appli

## ALIGNMENTS

RESULT 1 US-08-576-626A-31

Sequence 31, Application US/08576626A Patent No. 5998194

; GENERAL INFORMATION:		
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: APPLICANT: Staver.	<b>X</b>	
Ş	POLYKETIDE-ASSOCIATED	SUGAR
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€3	ESS:	
; ADDRESSEE: Abbott Laboratories	t Laboratories	
; STREET: 100 Abbott	tt Park Road	
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READABLE	FORM:	
TYPE: D	kette	
	IBM Compatible	
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; SOFTWARE: FastSEQ	Q Version 2.0	
CORRENT AFFLICATION OF	DAIA:	
; FILING DATE: 21-DEC-1995	٠	
; CLASSIFICATION:	435	
	ATA:	
; APPLICATION NUMBER:	<b>73:</b>	
CONTRACTOR CALLS	DWARTON.	
: NAME: Dianne Casuto	Casuto	
	ER: P-40,943	
; REFERENCE/DOCKET NUMBER:	Н	
; TELECOMMUNICATION INFORMATION:	NFORMATION:	
TELEPHONE: (847)	(847) 938-3137 (847) 938-3633	
N FOR SEQ	ID NO: 31:	
ACTE	STICS:	
• •	no acids	
; TYPE: amino acid		
; STRANDEDNESS: Si	single	
15	50081040	
; MODECOLE TIPE: NO.	399C194E	

Query Match

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Score 1728;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 307
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 962 LGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQ 1021
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                                                                          TOPOLOGY:
                                                                                     STRANDEDNESS:
                                                                                                    TYPE: amino acid
                                                                                                                                                            TELEPHONE: (312) 616-56
TELEFAX: (312) 616-5700
TELEX: 25-3533
                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                FILING DATE: 23-FEB-1996
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RLYKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 333; Conserv
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                          TYPE:
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                                         ; MOLECULE TYPE: US-08-606-143-3
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                                                                                STRANDEDNESS:
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                                                                     TOPOLOGY:
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                                                                                                               LENGTH:
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REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 7175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPAX: (312) 616-5700
TELEX: 25-353
INFORMATION FOR SEQ ID NO: 3:
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Matches 102; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Kilyk Jr., John
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, V
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STREET: INC
STREET: INC
TT.
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                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM .. COMPUTER: IBM .. PC-DOS/MU PATENTING SYSTEM: PC-DOS/MU PATENTIN Release #1.0,
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 23-FEE CLASSIFICATION: 514
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7; Mismatches 131;
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Pred. No. 1.1e-27; Mismatches

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                                             ; TOPOLOGY: 1; MOLECULE TYPE: US-08-606-143-2
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                                                                                                                                     TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Kilyk Jr., John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60601
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                                                                                                            TYPE:
                                                                                                                          LENGTH:
                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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Two Prudential Plaza, Suite 4900
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7; Mismatches 131;
 Score 331;
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US-08-907-674-1
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                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 WLKDKILSEEGRRQ------QAKLKELQAIAERLGCTLPQLAIAWCLRNEGVSSVLLGAS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 CLYNLAVRH-AELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAG------ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: FastSEC
TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                     NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 LVGRWLAQGGGRREDTVLATKV--GGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDV 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPEQLDSALKASAM--TLDEQALSELDEI 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLGNIIKKKGWRRSSLVITTKIFWGGKAE----TERGLSRKHIIEGLKASLERLQLEYVDV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
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3174 Porter Drive
                                                                      331 amino acids
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; LIBRARY: BRAINOT14
; CLONE: 1596452
US-08-907-674-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                     TELEFAX:
TELEX:
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CITY: Palo Alto
                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CO
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 EDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3174 Porter Drive
                                       415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bandman,
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                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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23.9%;
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Pred. No. 2.2e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ALRWMYHHSQLQGAHGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09391959 patent No. 6071704 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.1%;
Best Local Similarity 23.9%;
                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: BRAINOT14
CLONE: 1596452
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corley, Neil C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              STREET: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 ELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDGKQPVGRFFGNTWAEMYRNRYWKEHH 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AVILGMSSLEQLEQNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 -- VIGPRTPEQLDSALKASAMTLDEQALSELDEIFPAVASGGAAPEAW 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AAGTAV--KSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGA---
                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                              COMPUTER: IBM CONCERNING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LGAMEMGRRMDAPTSAAVTRAFLERGHTEIDTAFVYS----EQQSETILGGLGLRLGGGD 69
                                                        FILING DATE:
                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 CRVKIATK-----ANPWDGKSLKPDSVRSQLETSLKRLQCPQVDLFYLHTPDHGTPVEET 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 EDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRR 82
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                                                                                                                                                                                                                                                                            94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler, Karl J.
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                                                                                                                                                                                                                                        Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                               US/09/391,959
                                                                         08/907,674
 36,749
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Pred. No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AATEEGPLEPAVVD--AFNQAW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                SOFTWARE: FASTEEQ FOR WINDOWS VERSION CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
FILING DATE: Herewith
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
ITRRARY: BRAINOT14
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                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: BRAING CLONE: 1596452
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STRANDEDNESS: si
                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVILGMSSLEQLEQNL------AATEEGPLEPAVVD--AFNQAW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTAV--KSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMV---SHQCLYNLAVRHAEL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRVKIATK-----ANPWDGKSLKPDSVRSQLETSLKRLQCPQVDLFYLHTPDHGTPVEET 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEGIALVEKALQAAYGASAPSVTSA--
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                                                                                                                                                 94304
                                                                                                                                                                                         Palo Alto
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US-08-907-674-3
                                                                                                                                                                                                                                                      Sequence 3, Application Patent No. 5981244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                              STREET: 31.
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LIBRARY: Gen-
ONE: 433611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J
REGISTRATION NUMBER: 36
 COMPUTER:
                                                  ZIP:
                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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IBM Compatible
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APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Phan--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 TLQACHHVHQEGKFVELGLSNYVSWEVAEICTLCKKNGWIMPTVYQGMYNAITRQVETEL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23- LGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ASAMTLDEQALSELDEIFPAVASGGAAP-----EAW 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDRYWKEEHF-----NGIALV---EKALKTTYGPTAPSMISAAVRWMYHHSQLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALK------
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                                                                                                                                                                                                                                                                                                          Application US/09215087
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Pred. No. 4.2e-13;
9; Mismatches 14(
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OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:

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; LIBRARY: GenBa
; CLONE: 433611
US-09-215-087-3
                                                                                                                                                                                                                                       US-09-391-959-3
                                                                                                                                                                                  Sequence 3, Application Patent No. 6071704 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                  APPLICANT: Bandman, Olga
APPLICANT: Shah, purvi
APPLICANT: Guegler, Karl J:
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              276 TQGDAVILGMSSLEQLEQNLALVEEGPLEPAVVDAFDQAW 315
                                                                                                                                                                                                                                                                                                                                                 301 --ASAMTLDEQALSELDEIFPAVASGGAAP-----EAW 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TLQACHHVHQEGKFVELGLSNYVSWEVAEICTLCKKNGWIMPTVYQGMYNAITRQVETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 LPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLR----PAIEAY 257
                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 EDTV-LATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LGAMEMGRRMDVTSSSASVRAFLQRGHTEIDTAFVYA----NGQSETILGD-LGLGLGRS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCKVKIATKAAPMFGKT-----LKPADVRFQLETSLKRLQCPRVDLFYLHFPDHGTPIEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                          -----EKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
Palo Alto
                 3174 Porter Drive
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                                                                                        HUMAN AFLATOXIN
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                                                                                                                                                                                                                                                                                                                                                                                       -NGIALV---EKALKTTYGPTAPSMISAAVRWMYHHSQLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 196.5; DB 2; Pred. No. 4.2e-13; 9; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0362
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                                                                                          B1 ALDEHYDE
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                                                                                       Sequence 1, Application US/07941414 Patent No. 5376544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                      APPLICANT:
                                                       APPLICANT:
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                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                           120 TLQACHHVHQEGKFVELGLSNYVSWEVAEICTLCKKNGWIMPTVYQGMYNAITRQVETEL 179
                                                                                                                                                                                                      276 TQGDAVILGMSSLEQLEQNLALVEEGPLEPAVVDAFDQAW
                                                                                                                                                                                                                                      301 --ASAMTLDEQALSELDEIFPAVASGGAAP-----EAW 331
                                                                                                                                                                                                                                                                                                                                                                                     202 LPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLR----PAIEAY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 VWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GCKVKIATKAAPMFGKT-----LKPADVRFQLETSLKRLQCPRVDLFYLHFPDHGTPIEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 LGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                   FPCLRHFGLRFYAFNPLAGGLLTGRYK-----YQDKDGKN----PESRFFGNPFSQLY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDTV-LATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGAMEMGRRMDVTSSSASVRAFLQRGHTEIDTAFVYA----NGQSETILGD-LGLGLGRS 64
                                                                                                                                                                                                                                                                                                               -----EKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
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FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
ANDERSON, STEPHEN POWERS, DAVID B.
                                    LAZARUS, ROI
HURLE, MARK
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                                                       ROBERT A
                                                                                                                                                                                                                                                                            --NGIALV---EKALKTTYGPTAPSMISAAVRWMYHHSQLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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Gaps

12;

300

CORRESPONDENCE ADDRESS: TITLE OF INVENTION:

STREET: ADDRESSEE:

SAN DIEGO

11545 W. BERNARDO COURT, SUITE 302

FREDERICK W. PEPPER, PH.D.

NUMBER OF SEQUENCES:

ENZYMES FOR THE PRODUCTION OF 2-KETO-L-GULONIC ACID

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                                                                                                                RESULT 12
US-08-249-377A-1
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Best Local S
Matches 76
                                                                                 Sequence 1, Application US/08249377A Patent No. 5583025
                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
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                  APPLICANT:
                                                                                                                                                                                   266 GSG
                                                                                                                                                                                                                322 ASG
                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                264 LGEDPAEVGLAWVLSRPGIAGAVIGPRT--PEQLDSALKASAMTLDEQALSELDEIFPAV 321
                                                                                                                                                                                                                                                                                                               178 AAHDVKIESWGPLGQGKYDLFGAEPVTAAAAA----
                                                                                                                                                                                                                                                                                                                                                206 QAYGLGVFAWSPLHGGL--LSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRN
                                                                                                                                                                                                                                                                                                                                                                               124 MIELRAAGLTRSIGVSN----HLVPHLERIVA--ATGVVPAVNQIELHPAYQQREITDWA 177
                                                                                                                                                                                                                                                                                                                                                                                                                146
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 VGGEMSERVNDSGLSARH----IIASCEGSLRRLGVDHIDVYQMHHIDRSAP-WDEVWQA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 76; Conserv
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ZIP: 92127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 KVPPADTQRAVEEALEVGYRHIDTAAIYG-----NEEGVGAAIAASGIARDDLFITTK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 RVEDDDALRIMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRREDTVLATK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19920908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                 HGKTPAQAVLRWHLQK----GFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDPGD 265
                                                                                                                                                                                                                                                                                                                                                                                                                MDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               LW-----ND-----RHDGDEPAAAIAESLAKLALDQVDLYLVHWPTPAADNYVHAWEK 123
                                                                                                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPPER PH.D., FREDERICK W.
                                                                                                                                                                                   268
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ANDERSON, STEPHEN POWERS, DAVID B.
                                HURLE,
                                                LAZARUS, ROBERT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 4.3e-11;
4; Mismatches 117;
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                                                                                                                                                           RESULT
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                                                                                   Sequence 1, Application US/08585595 Patent No. 5795761 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
APPLICANT: POWERS, DAVID B.
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: IMPROVED
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                264
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                                                                                                                                                                                                              266 GSG
                                                                                                                                                                                                                                                                               210 HGKTPAQAVLRWHLQK----GFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDPGD 265
                                                                                                                                                                                                                                                                                                                                                                                 206 QAYGLGVFAWSPLHGGL--LSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 MDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 VGGEMSERVNDSGLSARH----IIASCEGSLRRLGVDHIDVYQMHHIDRSAP-WDEVWQA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1299 PEN CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                              LGEDPAEVGLAWVLSRPGIAGAVIGPRT--PEQLDSALKASAMTLDEQALSELDEIFPAV
                                                                                                                                                                                                                                                                                                                                                  AAHDVKIESWGPLGQGKYDLFGAEPVTAAAAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 177; DB 1; 25.1%; Pred. No. 4.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383-7451
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                                    METHODS FOR PRODUCING VITAMIN C
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RESULT 14
US-08-749-337-1
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Best Local Similarity
~~+~hes 76; Conserv?
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                GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: 1:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
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FILING DATE: 11-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
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PRIOR APPLICATION DATA:
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                                                                                                                                                                            322 ASG
                                                                                                                                                                                                                                                                                  178 AAHDVKIESWGPLGQGKYDLFGAEPVTAAAAA----
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                                                                                                                                                                                                                                                                                                                                                                                        146 MDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAA 205
                                                                                                                                         266 GSG
                                                                                                                                                                                                              210 HGKTPAQAVLRWHLQK-----GFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDPGD
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CITY: WASHINGTON
STATE: DC
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1299 PENNSYLVANIA AVENUE, N.W.
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25.1%;
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ROBERT A.
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Pred. No. 4.3e-11;
i4; Mismatches 117;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
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LENGTH: 278 amino acids
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                322 ASG
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                                                                          266 GSG
                                                                                                                                                    210 HGKTPAQAVLRWHLQK----GFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDPGD
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                                                                                                                                                                                  264 LGEDPAEVGLAWVLSRPGIAGAVIGPRT--PEQLDSALKASAMTLDEQALSELDEIFPAV 321
                                                                                                                                                                                                                                                             206 QAYGLGVFAWSPLHGGL--LSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRN 263
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OPERATING SYSTEM:
SOFTWARE: PatentI
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ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 RVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGRREDTVLATK 90
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Similarity 25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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383-6610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 177; DB 2;
Pred. No. 4.3e-11;
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Sequence 3, Application US/08336198C Patent No. 5866382 GENERAL INFORMATION: APPLICANT: Hallborn, Johan

209

APPLICANT:

Penttila, Merja

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TELEFAX: 703-205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-198C-3
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Best Local Similarity 23.5
Matches 70; Conservative
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NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,198C
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS
NUMBER OF SEQUENCES: 9
                       263 NLGEDPAEVGLAWVLSRPGIAGAVIGPRT---PEQLDSALKASAMTLDEQALSELDEI 317
                                                                                                                203 PAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCR 262
                                                                                                                                                                                                          146 MDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELE---VL 202 :: || :|| :| :: ::
                                                                                                                                                                              150 LEKLVKAGKIRSIGVSNFPGALLLDLLRGATIKPSVLQVEH------HPYLQQPRLI 200
247 KHGKSPAQVLLRWSSQR----GIAIIPKSNTVPRLLENK-DVNSFDLDEQDFADIAKL 299
                                                                                          201 EFAQSRGIAVTAYS-----
                                                                                                                                                                                                                                                                                                                 111 ASCEGSLRRLGVDHIDVYQMH-----------HID-RSAPWDEVWQA 145
                                                                                                                                                                                                                                                                        90 KALNRTLSDLQVDYVDLFLIHFPVTFKFVPLEEKYPPGFYCGKGDNFDYEDVPILETWKA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                   38 GYRLFDGAEDYANEKLVGAGVKKAIDEGIVKREDLFLTSKLWNNYHHPDN-----VE 89
                                                                                                                                                                                                                                                                                                                                                                                                              59 GWRLYKG----HTEELVG----RWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHII 110
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Hahn-Hagerdal, Barbei
Waldfridsson, Mats
Airaksinen, Ulla
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23.5%; Pred. No. 2.5e-09;
rative 49; Mismatches 104;
                                                                                     ----SFGPQSFVELNQGRALNTSPLFEN--ETIKAIAA 246
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Search completed: June 22, 2001, 09:24:49 Job time: 110 sec.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                         June 23, 2001, 10:02:37; Search time 1502.48 Seconds (without alignments) 10284.517 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 2 AF263245	$\vdash$	N	N	9	ω	9	9 3 SEY14332	SUMMARIES  Query  Query  And Descions and De
AF263245 Micromono	AB032523 Streptomy	AF147704 Streptomy	AF263245 Micromono	AR092721 Sequence	U77454 Saccharopol	AX000482 Sequence	Y14332 Saccharopol)	poly de les de la poly

gene complement(113)	(	University Of Cambridge, Tennis Court Road, Cambridge CB2 1QW, UK FEATURES Location/Qualifiers 1.3439	ssion 8-JUL-1997) P.F. Leadlay, Depar	erythraea Unpublished 2 (bases 1 to 3439)	TITLE Targetted gene inactivation for the elucidation of deoxysugar biosynthesis in the erythromycin producer saccharopolyspora	REFERENCE I (DASES I TO 3439) AUTHORS Salah-Bey.K., Doumith,M., Michel,J.M., Haydock,S., Cortes,J., Leadlav.P.F. and Ravnal,M.C.	Actinomycetales; Pseudonocardineae; Saccharopolyspora.	ORGANISM Saccharopolyspora erythraea Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	DEFINITION SACCHAROPOLYSPORA ERYTHRAEA PARTIAL ERYG AND ERYGIII and ERYGII genes.  ACCESSION 114332  VERSION Y14332.1 GI:2765405	SEY14332 3439 bp DNA BCT 24-JUL	ALIGNMENTS	N. T. CANTENING	44 92 9.2 2929 3 SCCLAVAM1 45 92 9.2 7193 9 A89635	95.2 9.5 332635 2 AP003005 AP003005 Mesoribi 92.4 9.2 347750 2 AP002998 AP002998 Mesoribi 92.4 9.2 1032 0 A80638 A80638 CONTROLOGICA	96.6 9.7 345783 2 AP003001 AP003001 95.4 9.5 13184 1 AE005096 AE005096	108.2 10.8 11104 1 AE004543 104.4 10.5 10307 1 AE004542	34 112.4 11.3 5413 3 HVU95374 U95374 Ha 35 111.8 11.2 346897 2 PROVENDETA APOO2995 I 36 109 3 10 8 084 14 ENVIOLETA APOCA	113.6 11.4 10948 1 AE004857	129 12.9 12021 1 AE005073 129 12.9 12021 1 AE005073 117 11 7 13201 1 AE005032	132.4 13.3 15586 3 SC7H9 AL450223 132.4 13.3 194140 2 AR242881 AR242881 AR242881	25 139.4 14.0 349498 2 AP003002 AP003002 26 135.6 13.6 7449 3 SCD17A AL392177	140.4 14.1 17148 1 AE004798 139.6 14.0 36583 3 SC5H1	21 150 15.0 1512 10 AX078635 22 147.2 14.7 12257 1 AF005963	19 167 16.7 145914 20 157.6 15.8 22134	1/9 1/-9 8038 3 SCE38 167.4 16.8 18495 2 BSUB3875 167.4 16.8 213420 2 BSUBDO14	14 185.2 18.5 10314 1 AE004600 AE004600 AE004600 15 180.8 18.1 349116 2 AP003003 AF003003 AF003003 AF1280E5	12 213.2 21.3 34074 3 SCF81 AL133171 13 208.4 20.9 39896 3 SCK13 AL451182 AL451182	22991 3 SCD19 AL392149 30657 3 SCD12A AL357524 12335 1 AE003996 AE003996
/cod	CDS comp	gene comp	LRGA SAEP VAAA	/tra YRSM FRDV	/db/ /db/	/tra /pro	/note= /codon	/gen /fun	DVDA GVPQ MRDD	FYAL ARQN TGLK	/db_ /tra AAGL	/pro /db_	/trans. /trans.	/fun /not	CDS comp	gene comp	SNFA HGGL	/ Lrd RDRG GLSA	/db/ /db/	/pro	/codon /trans	/fun /not	CDS comp	gene comp	/tra//	/pro	/funct /codon	/gen CDS /gen
/runction="involved in erythromycin A σιοδήπτωενικ /codon_start=1	401>3439)	GLTPSGPVVRRRRSPVLRGTNRCPVEL" Complement(34013439) /gong-"erva"	LRGAAWDARVSLDAQLSPQQLAVTEAAVAALPADPALRALFAGAEMTANTVVDAVLAV SAEPGLAERIADDPAAAQRTVAEVLRLHPALHLERRTATAEVRLGEHVIGEGEEVVVV VAAANRDPEVFAEPDRLDVDRPDADRALSAHRGHPGRLEELVTALATAALRAAAKALP	/translation="MTTDRAGLGROLOMIRGLHWGYSSNGDBYPMLLCGHDDDPQRR YRSMRESGVRRSRTETWVVADHATAROVLDDPATTARTGRTPEWMRAAGARPAEWAQP FRDYHAASWRGEVPDYGELABSFAGLLPGAGARLDLVGDFAWOYPVQGMTAVLGAAGV	/db_xref="GI:2765408" /db_xref="SPTREMBL:054225"	'transtable=11   product="dTDP-4-keto-6-deoxy-hexose 3,4-isomerase"   brotein id="CAA74711.1"	<pre>/note="putative" /codon_start=1</pre>	<pre>/gene="eryCII" /function="involved in desosamine biosynthesis</pre>	DVDAELIATEDAQQLEGVANIFDNVRTVGFVPMHALLPTCAATVHHGGPGSWHTAALH GVPQVILPDGWDTGVRAQRTQEFGAGIALPVPELTPDQLRESVKRVLDDPAHRAGAAR MRDDMLAEPSPAEVVGICEELAAGRREPR" COMPLEMENT (23193404)	FYALMSPDTLIEGMVSFCRKWRPDLVIWEPLTFAAPIAAAVTGTPHARLLWGPDITTR ARQNFLGLLPDQPEEHREDPLAEWLTWTLEKYGGPAFDEEVVVGQWTIDPAPAAIRLD TGLKTVGMRYVDYNGPSVVPEWLHDEPERRRVCLTLGISSRENSIGQVSIEELLGAVG	/dd_xreir="SPTREMBL:054224" /translation="MRVVFSSMASKSHLFGLVPLAWAFRAAGHEVRVVASPALTEDIT AAGLTAVPVGTDVDLVDFMTHAGHDIIDYVRSLDFSERDPATLTWEHLLGWQTVLTPT	/protein_id="CAA74710.1" /db_xref="61:2765407"	duct="qlycosyltransferase"	function="Involved in desosamine biosynthesis" 'note="putative" '/ode first-1	complement(10432308) /gene="eryCIII"	ייייייייייייייייייייייייייייייייייייי	SNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAMSPL HGGLLSALEKLAAGTAVKSAQGRAGVLLPSLKPAIEAYEKERKIGEDPAEVGLAW FGGLLSALEKLAAGTAVKSAQGRAGVLLPSLKPAIEAYEKERTANVSCGAANDAWIG	LIGHT AGUS TALLOH MILIMAN HYKLAKAALLIS NLWIGJ YNESOKY ELDUGALKLEUHK RDRGINCLDTADMYGWRLYKGHTEELUGRWILAGOGGGREEDTVILATK VGGEMSERVNUS GLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVAASGKVSYVGS	/db_xref="SpTrembL:033936" /rxref="SpTrembL:033936"	<pre>/product="dTDP-4-keto-L-6-deoxy-hexose 2,3-reductas /protein_id="CAA74709.1"</pre>	<pre>'codon_start=1 'transl_table=11</pre>	/function="involved in mycarose biosynthesis /note="putative"	complement(451046)	complement(451046)	/prottein_iq="CAA/4/08:1" /db_xref="GI:4388593" /translation="MSVK"	transl_table=11 product="0-mosy1700 1" restain id="casy1700 1"	<pre>function="involved in erythromycin A biosynthesis" codon_start=1</pre>	/gene="eryG" complement(<113) /gene="eryG"

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Mendez,C. and Salas,J.A.
BIOSYNTHESIS GENES AND TRANSFER OF
SACCHAROPOLYSPORA ERYTHRAEA AND IN
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB77091.1"
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VAAANROPEVFAEPDRLDVDRPDADRALSAHRGHPGRLEELVTALATAALRAAAKALP
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1 1233 C 1268 g 511 t
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LRGAAWDARVSLDAQLSPQQLAVTEAAVAALPADPALRALFAGAEMTANTVVDAVLAV
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/function="IMPLIQUE DANS
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/gene="ERYBII"
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                                                  SEU77454 3480 bp DNA BCT SEU77454 10.NOV-1997 SACCharopolyspora erythraea DEBSIII (eryAIII) and erythromycin O-methyltransferase (eryG) genes, partial cds, and ERYCII (eryCII), desosaminyltransferase (eryCII) and EryBII (eryBII) genes, complete
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Summers, R.G., Staver, M.J.
Hutchinson, C.R. and Katz,
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Summers, R.G., Donadio, S.,
Hutchinson, C.R. and Katz,
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Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Pseudonocardineae; Ps
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HGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGGDDAEVGLAWV
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Summers, R.G. Jr., Katz, L., Donadio, S. and Polyketide-associated sugar biosynthesis gpatent: US 5998194-A 1 07-DEC-1999;
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                                                                                                                                                     gene cluste:
AF263245
AF263245.1
    Micromonospora.

1 (bases 1 to 47981)

Volchegursky,Y., Hu.Z., Katz,L. and
Biosynthesis of the anti-parasitic
                                                                                                                                                                                                  AF263245 479
Micromonospora
                                                                                 Micromonospora megalomicea subsp. nigra.
Micromonospora megalomicea subsp. nigra
Bacteria; Firmicutes; Actinobacteria; Ac
                                                                     Actinomycetales; Micromonosporineae;
                                                                                                                                                                                   cluster, partial sequence
                                                                                                                                                     GI:10179840
                                                                                                                                                                                                  47981 bp DNA DNA subsp.
      and McDaniel,
tic agent mega
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                                                                                    Actinobacteridae;
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Mol. Microbiol.
20430101
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McDaniel,R. and Volch
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-MAY-2000) Kosan Place, Hayward, CA 94545, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transformation
   /product="TDP-megosamine glycosyltransferase"
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GAGLTAVPVGDDVELVEWHAHAGQDIVEYMRTLDWVDQSHTTMSWDDLLGMQTTFTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAVGDRRRLGRELQMARGLYWGFGANGDLYSMLLSGRDDDPWTW
YERLRAAGRGPYASRACTWVVGDHRTAAEVLADGGTHG9PDAARWMQVAHCPAASWA
GPFRREYARTEDAASVTYDDADWLQQFQCARLVTELGSRFDLYNDDFAREVPYLALGTAPA
LKGVDPDRLRSWTSATRVCLDAQVSPQQLAVTEQALTALDEIDAVTGGRDAAVLVGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928.
                                                                                                                                                                                 /gene="megY"
3462. .4634
                                                                                                                                                                                                                            AIADIDAEFVATFDDQOLVGVGSVPANVRTAGFVPMNVLLPTCAATVHHGGTGSWLTA
AIHGVPQIILSDADTEVHAKQLQDLGAGLSLPVAGMTAEHLRGAIERVLDEPAYRLGA
ERMRDGMRTDSPAQVVGICQDLAADRAARGRQPRRTAEPHLPR*
                                                                                                                                                                                                                                                                            FFALMSPDSLIDGMVEFCRSWRPDWIVWEPLTFAAPIAARVTGTPHARMLWGPDVATR
ARQSFLRLLAHQEVEHREDPLAEWFDWTLRRFGDDPHLSFDEELVLGQWTVDPIPEPL
RIDTGVRTVGMRYVPYNGPSVVPAWLLREPERRRVCLTLGGSSREHGIGQVSIGEMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="megDI"
2072. .3382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AELAANTVGNAVLAVTELPELAARLADDPETATRVVTEVSRTSPGVHLERRTAASDRR
VGGVDVPTGGEVTVVVAAANRDPEVFTDPDRFDVDRGGDAEILSSRPGSPRTDLDALV
ATLATAALRAAAPVLPRLSRSGPVIRRRSPVARGLSRCPVEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<1.
/gene="megT"</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="TDP-4-keto-6-deoxyhexose
/protein_id="AAG13907.1"
/db_xref="GI:10179842"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="NRRL3275"
                                                                                                                                                                  3462. .4634
/gene="megY"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="megDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation-"MGDRVNGHATPESTQSAIRFLTRHGGPPTATDDVHDWLAHRAAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ne="megDVI"
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/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                  ARAFVTALDHADALAGRHFLLGTGRSWPLGEVFQAVSRSVARHTGEDPVPVVSVPPPA HMDPSDLRSVEVDPARFTAVTGWRATVTMAEAVDRTVAALAPRRAAPSEPS" Complement (8228. . .9220)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="TDP-4-keto-6-deoxyhexose 3,5-epimerase"
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/db_xref="GI:10179846"
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ELSAESMVGLYLPVGMGHLFVSLEDDTTLVYLMSAGYVPDKERAVHPLDPELALPIPA
                                                                                                                                                                                                     complement(8228.
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6592. .7197
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FARAAYEQAFQRAGLSCSYVGHDLFSPGLFVGVAAEPGR"
HALERGVNCIDTADIYGWRLYKGHTEELVGRWFAQGGGRREETVLATKVGSSEMSERVN
DGGLSARHIVAACENSLRRLGVDHIDIYQTHHIDRAAPWDEVWQAAEHLVGSGKVGYV
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7220. .8206
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RDFSLDRRFDVVTCMFSSTGYLVDEAELDRAVANLAGHLAPGGTLVVEFWWFPETFRP
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5822. .6595
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PVVTDGNEHVFYVYVVRHPRRDEIIKRLRDGYDISLNISYPWPVHTMTGFAHLGVASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTTYWSYLLEYEREADILDAVQKVFASGSLILGQSVENFETE
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AHGARRDGRLAGTMSDAAAFSFYPTKVLGAYGDGGAVVTNDDETARALRRLRYYGMEE
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PLGLALFMIIPFLAVSLVLSWLLYRFVELPVMRNWARPASARRKPATEPEQTPSRR"
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CACCCCGTACGCCTGGGCGGCGGGCAGGACGTCCAGCTCGGGGTGGCGGACGGCCAGGTT
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                                                                         Submitted (30-APR-1999) Biochemistry, University Road, Leicester LE1 7RH, UK
                                                                                                    2 (bases 1 to 5908)
Bate, N. and Cundliffe, E.
Direct Submission
                                                                                                                                                                                                         The mycarose-biosynthe
                                                                                                                                                                                             of tylosin
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/translation="MSGMYVQLGRGATLVSRLWLGTVNFSGRVPDDQAIRLMDEALDR GVNCVDTADIYGMRLYKGHTEELVGRWLRGSGRRDDVLLATKVGEPMSDRVNDRGLSA RHVIRSCEASLRRLGVDHIDLTQMHRMDRTVRMDELWQAMDQLVASGKVRYIGSSNFA GWHLAAGQESAARRGSLGLVSEQCLYNLAVRHAELEVLDAARAYGIGVFAWSPLHGGL LSGALRKLAEGTAVKSGQGRAQRTLPALRDTIARYERFCARVGRDPAEVGLAWLLSRP
                                                                                                                                                       /translation="MPAVPREDOMITSACRYCGNRELLPYLDLGEQALTGYFPREREE
TYPSIPLELYKCSPOGCGLYQLRHTPDPGLMYGEGYGYRSGIRPFMIGHLRRKVAAIR
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DVFTARFGTRRARVITSIAMFYDLPDPLAFMRDVHDYLADDGIMVMEQSYLPAMLEAD
GPARIRARETEAKINTMAPFEEFARRVEHQRDALRDFLDRSRAAGRLTLGYGASTKGN
VILQYCGIGERDLPCIGEVSPEKAGRFTPGTGIPIVSEEDAKAMRPDQLLVLPWIYRE
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VARRPSPVPAGAVAEIEVRRRDLSLPGEVTEAVEDADAVVHLVAHTGGEKSWRAAGER
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RDLLDVRDAATAFTTALEHADQLRGKHWVVGTGRRHRLDRVFGTVAALAAEHTGRPPV
                                                                                                                     AYDIVCHEHLEYYALQQIEWMAERAGLTVLRAELTDVYGGSLCVT1.ARASSPHPRDEA
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                                                                                                                                                                                                                           CCGGTGGTGCCGGGCCGATCACCGCGCGCTGACACCGGGGCGGGACAGCAGCCAGGCG
                                                                                      ccgctggcgacgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcg
                                                                                                                                                                                                                                                                            AAGACCCCGATGCCGTAGGCGCGGCGGCCGGCAGGACCTCCAGCTCGGCATGGCGGACC
                                                                                                                                                                                                                                                                                                aagacgccgagccgtaggcctgcgggcgggcagcacctccagctcggcgtgccggacc
                                                                    CCGCTCGCCACCAACTGGTCCATCGCCTGCCAGAGTTCGTCCCAGCGTACGGTCCGGTCC
                                                                                                                                        TCCTGCCCGGCGAGGTGCCATCCGGCGAAGTTCGAGGACCCGATGTAGCGGACCTTT
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/protein_id="AAD41825.1"
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QDAESGVAVYLPDGLIGLGYVALADDTCMNYLYTREYTPGMIIDIDALDPGLGLPWNLT
EPPVRSERDAAAPSLAEAAAAGTLPGYEQCLRAYPAM"
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PRASFHGTWQRPEDGRPLVMVSLGTIYNERPGIFRACVEAFRDRPWNILLVLGGGLGA
GDLGPLPENVLVRDFVPLGDVLPHTDLLVNHGGTSTAMEALAHGVPIVAMPEMBPPRA
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/note="orf6*"
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75.9%;
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                                                                                                                                                                                                                                                                            Ikeda, School of Pharmaceutical Sciences, Kitasato University, Microbial Chemistry; 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan (E-mail: keda@mc.pharm.kitasato-u.ac.jp, Tel:+81-3-5791-6242,
                                                                                                                                                                                                                                                                                                                               Ikeda, H., Nonomiya, T., Usami, M., Ohta, T. and Omura, S. Direct Submission
Submitted (17-SEP-1999) to the DDBJ/EMBL/GenBank databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    Ikeda,H., Nonomiya,T., Usami,M., Ohta,T. and Omura,S. Organization of the biosynthetic gene cluster for the polyketide anthelmintic macrolide avermectin in Streptomyces avermitilis Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9509-9514 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-O-methyltransferase; dTDP-4-keto-6-deoxy-L-hexose2, 3-O-methyltransferase; dTDP-4-keto-6-deoxyhexose 3,5-epimerase; dTDP-4-keto-6-deoxyhexose; glucose-1-phosphate thymidyltransferase; dTDP-glucose 4,6-dehydratase; glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avermitilis avermectin (orfl, aveBI, aveBII, aveBIII, aveBI aveBIII), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis DNA.
Streptomyces avermitilis
                                                                                                                                                                                                                                                               Japan (E-mail:ikeda@
Fax:+81-3-3444-6197)
                                                                                                                                                                                                                                                                                                                                                                                                      99380548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transferase; reductase.
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                                                                                   /gene="orf-1"
/note="contains NAD(P)H
avermectin biosynthesis"
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/protein_id="BAA84591.1"
/db_xref="GI:5921155"
                                                                                                                                                                         /organism="Streptomyces
/db_xref="taxon:33903"
160. .873
                                                                                                                                        /gene=
160. .
                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRDAQVTGRRIÀELGLGRMVQPEEVTATTLRRHVLDIISDDAITRQVRQMQRATVEA
GGALRAADETERFLRRTRRH"
SEPDEPVTAYARQKLDAERTLKSATVEGVLRGISLRLPTVYGAGPGPQGNGVVQAMVL
RALADEALTVWNGSVVERDLVHVEDVAQAFVSCLAHADALAGRHWLLGSGRPVTVPHL
FGAIAAGVSARTGRPAVPVTAVDPPAMATAADFHGTVVDSSAFRAVTGWRPRLSLQEG
                                                                                 /translation="mGrfSvCpprpTgILKSmLTTGmCDrpLvvVLGaSGyIGSavaa
ELARWPVLLRLVARRPGVVPPGGAAETETRTADLTAASEVALAVTDADVVIHLVARLT
QGAAWRAAESDPVAERVNVGVMHDVVAALRSGRRAGPPPVVVFAGSVYQVGRPGRVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYGEYLMSIAAEAAVRSPGCAYS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVLGDNIFHGMGFSHLLRSHTRDVDGCVLFGYAVTDPERYGVGEVDASGKLLSVEEK
PTAPRSNLAITGLYLYDNDVIEVARGIRSSARGELEITDVNRAYLAEGRARLVDLGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTGGAGFIGSHEVRRLLTGAYPAFTGAEVVVLDKLTYAGRLENLAPVLGSPSLLTVHGDICDGPLVADLMDGSDMVVHFAAESHVDRSVADAAEFVRNVLGTHTLLRAATDAAVDREVY ISTDEVYGSIDSGSWTVHFAAESHVDRSVADAAEFVRDWLHARSFHTLLRAATDAAVDREVY ISTDEVYGSIDSGSWTEDAPLEPNSPY SASKASSDLLARSFHTEIGLPV ITTRCSNNYGPHOFPEKLIPRFVTHLLNGTKVPLYGDGENVRDWLHVDDHCRGIALVAERGRPGEIYHIGGGTELSNRELTARLLDLLGVDWSMVEPVTDRKGHDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2075. .3142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MCVDRDGRGAGVTADLARTRGARAAWPEVADVSDGAAMERFAER
/AETYGVVDLLVNNAGIGMAGRFLDTSVEDWQRTLGVNLWGVIHGCRLIGRQMAERGQ
VAETYGVADLAAAFQPTRAVPAYATSKAAVLMLSECLRAEFAERGVGVSVVVCPGFVRTS
GGHHVTVASSAAAFQPTRAVPAYATSKAAVLMLSECLRAEFAERGVGVSVVTVTAEARLSRL
FASAMHFAGVPRLEQERLRALFAGRGCSAEKVAAAVLRSVARDSAVVTVTAEARLSRL
                                                                                                                                                                /product="dTDP-4-keto-6-deoxy-L-hexose 4-reductase"
/protein_id="BAA84595.1"
/db_xref="GI:5921159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTWLDAGTHDSLMHAGQYVQVLEKRQGVRIACLEEIAFRMGLIDADDCYLRGVELAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="glucose-1-phosphate thymidyltransferase"
/protein_id="BAA84594.1"
/db_xref="GI:5921158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3139. .4038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="aveBIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3139. .4038)
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ARSRPLPAGRRPPRPWPAASA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="aveBII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2075. .3142)
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/protein_id="BAA84592.1"
/db_xref="G1:5921156"
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                                                                                                                                                                                                                                                                                                             note="function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="dTDP-glucose 4,6-dehydratase"
/protein_id="BAA84593.1"
/db_xref="GI:5921157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="function in oleandrose biosynthesis"
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DHGLDPAHYGMAWYLSRPGYTGLYIGPRTEQHYDGALHALRTPLPEPYLARLEELFPP
VGRGGSAPDAWLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNVQARTLLSLLTTRAVEL® complement(7394..81
                                                                                                                                                                                                                                                                                /translation="mmpttaepapvQSDSNSSAplhtelGrtrlrisrlalGtvN1GG
RVEEPEARRLMDHALAQGITLFDTANTYGWRVHKGYTEEVIGRWLADRPARREQVVLA
TKVGDPMGSGPNDHGLSVRNIVAACDASLRRLRTDWIDLYQLHHIDRRAGWDEVWQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8254. .9297)
/gene="aveBVIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIGFDTFTGFPDIDEADEVSTSAVPGRFAVPDGEVEHLRQVLAAHEANEPYGHTQRSF
VVQGDVRETVPQYLAEHPHTVIALAYFDLDLYRPTRELLDVITPHLTRGSILAFDELT
HPKWPGETRALSEAFGLDHAPLRQLPGREPPVIYMTWGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLGQIGELMHRDNLVNMDARTVLACLPTPFDEPAALHSDAELLSWYAAERSRHSVHA
RRVPLAGIPGWTTGAESIAHHADRYFRVVAVRVEASNREVAAWTQPLIEPCGHGITAF
LTRRIGGVPHLLAHGRVEGGFLDTIELGPTVQYTPRNYAHLTGPARPRFLDLVLEAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSVRADADHTEPSTAHRAARRRPARVPHPLRRRGRHRRRTSLDA
FTGMWTRRSCAHRFRYERIPFHGMDAWSFHPGTGNLAHRSGRFESVEGLHVRGGEOPF
PETGMWTRPAGAHRFRYERIPFHGMDAWSFHPGTGNLAHRSGRFESVEGLHVRGGEOPF
PETGMWTRRSCAHLAKKFDGVLHFLMQAKMEFGRINLVGLSPTYQATRSMYTK
VHGGAAVKYLEYFTQPRRATVVVDVLQSEHGAWFHRKFNRNIVVETDEDVPLDDDFRW
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                                                                                                                                                                                                                                                     DLLITQGKVRYVGSSNFAGWDIASAQEAARRRNALGLASEQCVYNLVTRHAELEVIPA
                                                                                                                                                                                                                                                                                                                                                                  /product="dTDP-4-keto-6-deoxy-L-hexose 2,3-reductase"
/protein_id="BAA84599.1"
/db_xref="GI:5921163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVYMRRNQLADLLSMDALYRMLPEVPGVIMEFGVLHGRHLATLTALRSIYEPYNSLRR
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/protein_id="BAA84597.1"
/db_xref="GI:5921161"
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/protein_id="BAA84598.1"
/db_xref="GI:5921162"
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ARGRALDFVVDLRTGSPTFGQWDSVLLDQERFRSVYLPIGVGHAFVALEDDTAMVYLM
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/protein_id="BAA84596.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Volchegursky,Y., Hu,Z., Katz,L. and McDaniel,R. Biosynthesis of the anti-parasitic agent megalomicin: transformation of erythromycin to megalomicin in sacc
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Micromonospora megalomicea subsp. nigra
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/db_xref="GI:10179841"
/d
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VGGVDVTTGGEVTVVVAAANRDEVFTDEDRFDVDRGGDAEILSSRPGSPRTDLDALV
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928. .2061
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                                                                                                                                                                                                                                                                                                                                                   /gene="megDI"
2072. .3382
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                                                                                                                                                                                                                                                                                                                            /gene="megDI"
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THRVDLTEPGALAEVVADARAVFPFAAQIRGTSGWRISEDDVVAERTNVGLVRDLIAV
LSRSPHAPVVVFPGSNTQVGRVTAGRVIDGSEQDHPEGVYDRQKHTGEQLLKEATAAG
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ELSAESMVGLYLPVGMGHLFVSLEDDTTLVYLMSAGYVPDKERAVHPLDPELALPIPA
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YARYHGIAHCYGVDNGTNAVKLALESYGVGRDEVVTVSNTAARTVLALDEIGARDVF
VDVRDEDYLMDTDLVEAAVFPRTKALVFYHLYGOCVDMTALRELADRRGLKLYEDCAQ
VDVRDEDYLMDTDLVEAAVFPRTKALVFYHLYGOCVDMTALRELADRRGLKLYEDCAQ
AIRATSLRLPPVFGVPAAGTADDRGVVSTMIRRALTGQPLTMWHDGTVRRELLYVTDA
ARAFVTALDHADALAGRHFLLGTGRSWPLGEVFQAVSRSVARHTGEDPVPVVSVPPPA
                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="TDP-4-keto-6-deoxyhexose
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7220. .8206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLDLVMSERDRVAPTLREARDQGILPDYAACRAAAHRVVRT"
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6592. .7197
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RDF SLDRRFDVVTCMFSSTGYLVDEAELDRAVANLAGHLAPGGTLVVEPWWFPETFRP
GWVGADLVTSGDRRISRMSHTVPAGLPDRTASRWTIHYTVGSPEAGIEHFTEVHVMTL
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VYYVTRTPGHNSRLDEVQAEILRRKLTRLDAYVAGRRAVAQRYVDGLADLQDSHGLEL
PVVTDGNEHVFYVYVVRHPRRDEIIKRLRDGYDISLNISYPWPVHTMTGFAHLGVASG
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YAAGGLAFMQTTGRYGVSFFFILSGFYLTWSARASDSVWSFWRRYCKLEPNHLYTAF
AANVLFLYTGOAVSGEALLIPNLLLHAMEPALEISFGINPUSWSLACBAFFYLCFFF
AFWISGIRPERLWAWAAVVEAAIWAVPVVADLLLPSSPPLIPGLEYSAIODWFLYTFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="TDP-4-keto-6-deoxyhexose 3,5-epimerase"
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LVLIIASGATADLQQKRTFMRNRVMVWLGDVSFALYMVHFLVIVYGADLLGFSQTEDA
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/groduct="daunosaminy1-N,N-dimethyltransferase"
/grotesin_io="AAGi3912.1"
db_xref="G1:10179847"
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/transl_table=11
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|651. .5775
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protein_id="AAG13909...
/db_xref="GI:10179844"
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Best Local Similarity.
Matches 697; Conserv
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gagccccacctcggccgggtcttcgccgaggttgcggcagaacttctcgtaggcctcgat 240
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                                                                                                 ctcgggggttcgcgggccgatgacggcgcggcggtgccggggccgggacagcacccatgc
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FDGEIVVTRSGLDPASVPDNVRLVDFVPMNILLPGCAAVIHHGGAGSWATALHHGVPQ
ISVAHEWDCVLRGQRTAELGAGVFLRPDEVDADTLWQALATVVEDRSHAENAEKLRQE
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VFPVVNNDSFVDELVEFAMDWRPDLVLWEPFTFAGAVAAKACGAAHARLLWGSDLTGY
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HALERGVNCIDTADIYGWRLYKGHTEELVGRWFAQGGGRREETVLATKVGSEMSERVN
DGGLSARHIVAACENSLRRLGVDHIDIYQTHHIDRAAPWDEVWQAAEHLVGSGKVGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTRHVTLLGVSGFVGSALLREFTTHPLRLRAVARTGSRDQPPGS
AGIEHLRVDLLEPGRVAQVVADTDVVVHLVAYAAGGSTWRSAATVPEAERVNAGIWRD
LVAALRARPGPAPULLFASTTQAABPAPSRYAQHKIEAERILRQATEDGVVDGVYLL
LPAIYGHSGPSGQTGRGVVTAMIRRALAGEPITMWHEGSVRRNLLHVEDVATAFTAAL
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/gene="megDVII"
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/product="TDP-4-keto-6-deoxyhexose 4-ketoreductase"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="TDP-mycarose glycosyltransferase"
/protein_id="AAG13915.1"
/db_xref="GI:10179850"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="megBV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="megAI"
/note="polyketide synthase"
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12181. .22821
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/db_xref="GI:10179851"
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/protein_id="AAG13914.1"
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                                                                                                                                                                                                                                                                                                                                                                                          48.78;
69.98;
                                                                                                                                                                                                                                                                                                                                                                    Score 486.2; DB 2;
Pred. No. 2.7e-44;
0; Mismatches 273;
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    TCGTCCTGGCCGGCGAGGGCTGCCGTACCCAGCCAGAGCCGGCTGGTCAGCAGGGCGCA

                                                                                                                   ABC transport system ATP-binding protein; ABC transport system integral membrane protein; aminotransferase; DNA invertase; integral membrane protein; integrase; nucleotidyltransferase; oxidoreductase; oxidoreductase lipase; tetR family transcriptional regulatory protein; two component system response regulator; two component system sensor kinase. Streptomyces coelicolor A3(2).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Kieser, H.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                correct initiation codon. Where possible we choose an initiatic codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the matter than the codon of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-SEP-2000) Streptomyces coelicolor sequencing projusanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A set of ordered cosmids and a detailed genetic and physical for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlapping sections once, or longer, because we arrang small overlap between neighbouring submissions. Cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usually the highest scoring match found by fasta -o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        upstream initiation codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jun/cgi-bin/frameplot.pl. CAUTION: We may not have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCD19.01c"
/note="SCD19.01c, unknown(fragment),
Contains two TTA leucine codons, pos
                                                                                                                                                                                                                                                 /product="hypothetical
/protein_id="CAC08302.1
/db_xref="GI:10129747"
                                                                                                                                                               SYLDGLFYPVREKLDEM'
                                                                                                                                                                                       GGGEKLKNEEMAEALRTLKFLLLRLKIDLKAPFDDFQSFRKYWIREGMGGGGGYAKRR
                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                    regulation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<1. .358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SCD19.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                               note="nominal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cosmid D19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="A3(2)
                                                                                                                                                                                                                             translation="MQRYGLKTELVDRLCNGPLEGVTDLEAAQALTRLVHTELENNGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 to 22991)
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                                                                                           overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2)"
                                                                                           Streptomyces coelicolor cosmid
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                                                                     complement(3196...4911)

/gene="SCD19.04c"
/gene="SCD19.04c"
/note="SCD19.04c, hypothetical protein, len: 571 aa;
/initar to some plasmid derived hypothetical proteins,
e.g. TR:085872 (BMBL:AF079317) Sphingomonas
aromaticivorans hypothetical 65.3 kDa protein (plasmid
pNL1), 595 aa; Tasta scores; opt: 344 z-score: 399.6 E()
9.4e-15; 26.7% identity in 561 aa overlap. Contains two
TTA leucine codons, possible targets for bldA regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1028..3199)
/gene="SCD19.03c"
/gene="SCD19.03c, hypothetical protein, len: 723 aa;
/note="SCD19.03c, hypothetical proteins hypothetical proteins,
similar to some plasmid derived hypothetical proteins,
e.g. TR:085873 (EMBL:AFF079317) Sphingomonas
aromaticivorans hypothetical 81.3 kDa protein (plasmid
pNL1), 741 aa; fasta scores: opt: 421 z-score: 478.1 E():
4e-19; 29.7% identity in 758 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLANCLYLLETTGPLLVPEAAAARAADOHEAASRRSLLVTEVDGLREEVERRRETGLP
ASRATEATVTORLKRGWDPGDPLLHMSWHPLVVQAAGAMGHROLETLREELERWYSE
CGLQOPWCRDAAPVPREDGTPVPWALPMARHOLDAMYVVTSAAYFITSALSGURSS
ELAELTSGCRROEERTGGGTRYRLVSRRIKGEAFGGTEDAWVVTEDVQRAIAIAEALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein SCD19.02c"
/protein_id="CAC08303.1"
/db_xref="GI:10129748"
/translation="wrinHQREAETRIRSAMORLLAGSVPDGLKCDVKSLCTLAGVPR
ATLYRTYPHLKAEFDRORTAAQDAGQQPDTRLAQIERLKAEVATLRERLSRKNVELDA
LKEFQVTALSKIAAQDDAITSLRRELEAAQERRLRPVPRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(603. 1031)
/gene="SCD19.02c"
/note="SCD19.02c, unknown, len: 142 aa. High content in alanine, arginine and leucine amino acid residues"
                                                                                                                                                                                                                                                                                           complement(3196. .4911)
/gene="SCD19.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAPGERLFAKASNNSGRRYTALSSWVNDEYGQRLGLEPLPDGPVNPRALRRTLAMA I
AQRPHGLMAVKLHLKHLSVATAEGYAARPGGHQAAFAAEVAAEEEAEHLRLTVAAYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MITAHASSPALAGRRPFHGLPVIETAGLRREPGSPRPVFDQDVW
DLTGLADAPVVMSTHRKILDFTAIINFESLSQVRGHCDAYLAAASRSATDDRLLSPAF
LNPMSLWSELHALALMFMHLTAVGITGSLSQVRGHCDAYLAAASRSATDDRLLSPAF
TVAMVRIPQFLVLXAEILSDCYQPGFAPWQGRSADEVTGYVRSDENRVPPVPDTLLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCD19.03c"
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complemen+/^^-
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                                                                                                                                                                                                                                                                                                                                                                                         FLGNPRLSKPERARAQNAFERATRIVAEIDAAGHPVEELHS'
                                                                                                                                                                                                                                                                                                                                                                                                                  NYCWFSDPSKALCLKLAGTPDADEPLIGMCDSARCPQATHHSQHRQIWADHADNTQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                          YQRGILPSGQGARDLVAAFKSVDQALERHDAGPVTVIDDRRVERVLKAKAKTLHLGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="CAC08304.1"
/db_xref="GI:10129749"
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/note="TTA leucine codon.
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/note="TTA leucine codon.
regulation".
/label=TTA
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       /product="hypothetical protein'
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                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                    282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 cggggaagatctcgtccagttcggacagcgcctgctcgtccagggtcatcgcggacgcct 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | tcagcgcggagtcgagctgctcggggggttcgcgggccgatgacggcgccggcggcggcggtgccgg 161
agtgg---cggcgggcgttctcctgcgcggcggcggtgtgccagcccgcgaagttcg
                                                                     gccgggacagcacccatgcgagccccacctcggccgggtcttcgccgaggttgcggcaga 221
                                                                                                                                                                                             cytycaycygcyaccayycyaayacyccyaycccytayycctycycygygygygcaycacct 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCGCCGAGTCCAGCTGCTGCGTGCGGGGGCCGACAATCGGGGCCGGTCACGCCGG
                                                                                                                                                                       CGTGCAGCGGCGACCACGGGATGACCCCGAGCCCGTAGTCCCGCGCGGGCCGGGATCACCT 7640
                                                                                                                                                                                                                                                                     GGCCGCTCGCCCGGCGCCCTGTGTGGCCTCCTTCTTGATCACGCCGCCCAGCAGAACCGC 7700
                                                                                                                                                                                                                                                                                                     gcgccgacttcaccgcggtgcccgcggccagcttctccagcgctccgctgagcaggccgc 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGGGTGAGCCAGCCAGCCAGCCGCCCTCGCCGGGCTGCAGGCCGTGCTTGTCGAGCA 7820
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7580

7880

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Similarity
  Conservative
                                                                                            complement(4911. .6263)
/gene-"SCD19.05c"
/note-"SCD19.05c, possible integrase, len: 475 aa; highly
/note-"SCD19.05c, possible integrase, len: 475 aa; highly
similar to TR:Q9RAJ3 (EMBL.AJ250372) Mycobacterium sp. GP1
putative integrase IntM, 451 aa; fasta scores: opt: 2152
z-score: 2497.3 E(): 0; 72.8% identity in 441 aa overlap"
                                                                                                                                                                                                complement(4911..6263)
/gene="SCD19.05c"
complement(4911..6263)
                                                                                                                                                                                                                                                                                                                                         /gene="none"
complement(3991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="none"
complement(3979.
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AVSALLSGEQDMFVAACASPLNGPHAPAGTLCPARPWVCLLCPLAAFAPRHLPNLLRL
                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                /note="TTA leucine codon. Possible target for bldA
regulation"
                                                                                                                                                                                                                                                                                                                        /gene="none"
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/db_xref="GI:10129750"
                   37.4%;
63.5%;
  0;
Score 374; DB 3;
Pred. No. 3.1e-32;
0; Mismatches 335
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    335;
                                   Length 22991;
15;
Gaps
2;
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                         TITLE
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by the BBSRC a
Details of S.
Details of S. coelicolor sequencing at available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/
                                                                                               Colney, Norwich, Norfolk NR4 Notes:
                                                                                                                                                                     Submitted (01-JUN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cold shock protein B; DNA helicase, pseudogene; hydrolase; integral membrane ATPase; integral membrane efflux protein; integral membrane protein; integrase; lipoprotein; marR-family protein;
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AL357524
                                                                                                              CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                      Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                          Seeger, K.J.
Unpublished
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A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                          and Beowulf Genomics
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     .sanger.ac.uk/Projects/S_coelicolor/)
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                                         the Sanger Centre
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jun/cgi-bin/framepiot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pp before the initiation codon). If this cannot be identified we choose the upstream initiation codon.

If the way not be identified we choose the most upstream initiation codon.

If may be shorter because we only sequence sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid D12A lies between and overlaps cosmids D95A and D19 on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database.
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The more significant matches with motifs in the PROSITE database may be fortuitous.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCD12A.02c"
complement(1407..1589)
/gene="scr"?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<1. .1328)
/note="SCD12A.01c, DNA helicase,
bp; similar to TR:053873 (EMBL:A</pre>
/note="SCD12A.03c, TBparse predicted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF00270 DEAD, helicase, score 22.40, E-value 3.6e-06"
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                       /gene="SCD12A.03c"
/note="scr)??
                                                                               /gene="SCD12A.03c"
complement/167
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/translation="MRGKTPTPGPDRSADRTTARSAVAVSVAALITAAALFGALAPKA
                                                                                                                                                                                                                                                                                                                                                                                                   spanning
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/note="scri?"
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/strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                     AALEGPLVNNINIALP"
                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                      residues
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCD12A.02c, possible integral membrane protein, len: 60 aa. Contains possible hydrophobic membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=pseudogene
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complement(1987. .4590)
/gene="complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSTEEKSAAPRSLAEALRVRDDVSLAALLRSRPDLITPVPTDLT QLATRAGTRASVVRALERLDREALQTAEALAVAPDEASYGELALMGGDEQDPAVAAA LPRAAALLREQALVWGADDRLRLVRTARELLANPSPQHPSPTGLGPTVREATAGMSPPG [QDILAAVGLDSTHDAYSAVSALGSLEADRRWAALLAELPWESREVLDRLVWGPPGF QVTHDPAAHLRALLDRGLLPTAPGTVVLPREVALHLRAGRAHRAPEPVPPQVEAAAT
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/note="SCD12A.06, possible hydrolase, len: 220 aa; simil note="SCD12A.06, possible hydrolase, len: 220 aa; simil to TR:086530 (EMBL:ALU31124) Streptomyces coelicolor putative hydrolase SCIC2.30, 244 aa; fasta scores: opt: 128 z-score: 155.4 E(): 0.34; 32.9% identity in 167 aa overlap. Contains Pfam match to entry PF00702 Hydrolase, placed dehalogenase-like hydrolase*
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IVTAAGGASGVRQQAAPSPTAVPEQRDTGPRDAARRKGRRSPAPETPAAPPAASPPHL
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/protein_id="CAB93396.1"
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/note="SCD12A.05, possible hydrophobic membrane spannir
366 aa. Contains possible hydrophobic membrane spannir
regions at C-terminal domain. High content in alanine,
arginine and glycine amino acid residues"
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TEPAAPQTPVEEAEEPTAGAVGKRAARRLPRLWPEGGWNNPLLLLAAALLTVGAVLGS
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/protein_id="CAB93395.1"
/db_xref="GI:8249974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MRTAVRRAATVLTSTAALLAAFAAEAAAVGIDLGGGLTL"
                       /product="putative hydrolase"
/protein_id="CAB93397.1"
/db_xref="GI:8249976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="6x degenerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPLGLGWLIAYLSRRLTPAQSKWAVLGLPGTVAAAGVVWLWGRTEGRWGDPVAEGHM
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                                                                                                            transl_table=11/
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translation="MASTTRPAPTVGFDLDMTLIDSRPGIRACYVELSARTGTYVDAD"
                                                                                                                                            codon_start=1
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Query Match
Best Local Sim
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gtggtcgacgcccagcctgcgcagcgatccctcgcaggaggcgatgatgtgccgcgcga
                                                                                                                                                                                                                                      ctgccacacctcgtccccacggcgcggaccggtcgatgtggtgcatctggtagacgtcgat
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                                                        CAGCTTGTCGTGGTTGGGCCACGCCTCGCCGTCGGCGCCCATGTTGCCGTACACCTTGGT
                                                                                               cagcccgctgtcgtt--
                                                                                                                                     GTGGTCGGTCTGGAGCCGCTTGAGGCTGGCATCGACCGCACGCCGAATGTTCACGGCGGA
                                                                                                                                                                                                                CTGCCAGATCTCGTCGAAGCCGGTGGCGCGCTCGATGTGGTAGAACTGGTAGAGGTCGAT 23976
                                                                                                                                                                                                                                                                                             GGGGAAGTTCGACGACCCCGCGTACAGCACCTTGCCCTGCTGGACCAGGGTGTCGATCGC
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/gene="SCD12A.07c"
/gene="SCD12A.07c"
/note="SCD12A.07c"
/note="SCD12A.07c"
/note="SCD12A.07c"
/note="SCD12A.07c"
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GGRAVVVTAKYEPNAKLHLAHLGIEPDAVIGGLWAEQKAVALREHDADVYVGDHVGDV
RGARAAGARSVAVASGPCDAGELRAAGADVVLADLTAFPEWLAAYRDGEGDAEGLDAA
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/note="Pfam match
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Pred. No. 2.1e-29;
0; Mismatches 271;
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28.00, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24097 GGCGATGACGGTCCTGTCGCCGCCGGTCGCCCTGGGCGAACCAGTTGCCGAGGATCTC 24156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S., Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C., Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C., Frenca,S.L., Gruber,A., Ho,P.L., Hohelsel,J.D., Junqueira,M.L., Kemper,E.L., Kitajima,J.P., Krieger,J.E., Kuramae,E.E., Laigret,F., Lambais,M.R., Leite,L.C.C., Lemos, E.G.M., Lemos,M.V.F., Lopes,S.A., Lopes,C.R., Machado,J.A., Machado,M.A., Madeira,A.M.B.N., Madeira,A.M.B.N., Madeira,H.M.F., Marino,C.L., Marques,M.V., Martins,E.A.L., Mardins,E.M.Y., Martins,E.M.F., Marins,E.M.Y., Marck,C.F.M., Miracca,E.C., Miyaki,C.Y., Monteiro-Vitorello,C.B., Moon,D.H., Nagai,M.A., Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.A., Nobrega,F.G., Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C., Palmieri,D.A., Paris,A., Peixoto,B.R., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Pereira,G.A.G., Gens,G., Santelli,R.V., de M.R., Marca,A.J., de Silva,A.R., G., Santelli,R.V., Jana, M.A., de Silva,A.R., Jana, Silva,F.R., da Silva,A.M., Silva,F.R., da Silva,A.M., Silva,F.R., da Silva,A.M., Silva,F.R., da Silva,A.M., Silva,F.R., da Silva,A.A., de Souza,A.P., Terenzi,M.F., Truffi,D., Tsai,S.M., Vettore,A.L., Zago,M.A., Zatz,M., Meidanis,J. and Setubal,J.C., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCGGTACGGCCCTTGTTCTCGCCCCAGCCGTACACATTGGCGGTGTCCA 24206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silvestri, M.L., Siqueira, W.J., de Souza, A.A., de Souza, A.P., Terenzi, M.F., Truffi, D., Tsai, S.M., Tsuhako, M.H., Vallada, H., Van Sluys, M.A., Verjovski-Ahmeida, S., Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubai, J.C.

The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvas, M.C., Araya, J.E., Bala, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C.R., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xylella
Xylella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE003996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 12335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 12335)
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                                                 /note="similar to GI|1934634 (percent identity: 55 %/query alignment coverage: 89.2 %/subject alignment coverage: 102.2 %); identified by sequence similarity; putative; ORF
                                                                                                                                                  complement(115. .1203)
/gene="XF1723"
                                                                                                                                                                                                             complement(115. .1203)
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/db_xref="taxon:2371"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
   located using Glimmer/RBSfinder/Start
/codon_start=1
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142 of 229 of the
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                               codon shift:
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                                                                                                                                                                                                                                                                                                    gene
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/gene="XF1726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2494. .2742)
/gene="XF1725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1437. .2426)
/gene="XF1724"
                                                                                                                                                                                                                                         complement(3709. .4770)
                                                                                                                                                                                                                                                                                                 complement(3709. .4770)
                                                                                                                                                                                                                                                                                                                             RAGRPEEIASAVLWLCSPGGSYVIGEGLTVDGGYVVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2758. .3525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAF84534.1"
/db_xref="GI:9106793"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2494. .2742)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1437. .2426)
/product="NADP-alcohol dehydrogenase
                                                    /codon_start=
                                                                                                                                                                                                                                                                     /gene="XF1727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF84535.1"
/db_xref="GI:9106794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="XF1726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="XF1725"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNLSSETLAKLDEIWPGPGGEAPKAYAW"
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/protein_id="AAF84532.1"
/db_xref="GI:9106791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/note-"similar to SP|P14941 (percent identity: 42 %/query alignment coverage: 100.0 %/subject alignment coverage: 100.3 %; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"similar to SP|P50197 (percent identity: 39 %/query alignment coverage: 97.3 %/subject alignment coverage: 99.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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KYLSAYHIRRACEASLKRLKTDHIDLYQMHHIDRATPWEDIWJAAFEQLIREGKITYVG
SSNPAGWIALAQCTARSRNLLGLASEOSLYNLTQRTIELEIIPALRHEFGIGLIPWSF
IGMGLLGGVLKKIASGRRATPGLQAQIDKLRPQLEAYEALCDELGQTPADVALAWLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                          RAAQEAAAIVAEGGTAIGLACDVSDEAQVAALVEKTVAEYGRLDFAFNNAGVMAKIAP
FAEATSEEFDRVIGINLRGVWLCMKYELQQMQRQGSGVIVNNASVGALTGNVGIGAYI
ASKHGVLGLTRAAALEYCKKGIRVNAVNPGTIDTQIARDVVGGSDEAFAKLGASAPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPHIIVKIAEGRSQPLKQELADRLAATMMDVLGLDSSAVSVAVE.
DVPMQDWMQQVYGPDIETAGERLLKRPGYGQLASPPEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPVVTAAISGPRTVEQLQQNLNALSVKLSDETLAKLDEIWPGPGGEAPQAYAW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q1QKFRPQLEAYEALCRELGQPPAVVALAWV1HNPVVTAA1SGPRTVEQMRENLKALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MNPTYDFKGQVALVTGAAAGMGLATARGFAQGGASVVLADRDGE/
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similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="sugar-phosphate dehydrogenase"
/protein_id="AAF8453.1"
/db_xref="GI:9105792"
/translation="MNYTHLGRTGLKVSRIALGTMNFGELTDEATSFKIMDTALDAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GI|1934634 (percent identity: 55 %/query alignment coverage: 98.2 %/subject alignment coverage: 102.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYIGRWLAQDKSRRDRIVLATKVYQPMGTGPNDKYLSAYHIRRACEASLKRLKTDHID
LYQMHHVDRSTPWQEIWQAMEQLVREGKITYVGSSNFAAWDIARAQGVAESRNFLGLV
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Query Match
Best Local
                                                                                                                                                                         Matches
96
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                                                                       117
                                                                                                                                                                                                 Local Similarity
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               acagegeetgetegteeategeggaegeetteagegeggagtegagetgetegg
                                                                                               accaggcttccggcgcgcgcgcggaggccaccgcgggggaagatctcgtccagttcgg
                                                                    ACCAGGCATAGGCCTTGGGTGCCTCGCCACCCGGGCCAGGCCAAATCTCGTCCAGCTTGG
                                                                                                                                                                         Conservative
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/protein_id="AAF84539.1"
/db_xref="GI:9106798"
                                                                                                                                                                                                                                                                                                                                                                                                                           alignment coverage: 96.6 %/subj. 94.1 %); identified by sequence: jocated using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7165. .8055)
/gene="XF1730"
complement(7165. .8055)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKLDASLSGQFAIGGDLTVNRLGFGAMRITGPDVWGEPEDHDEAIRVLKRLPEIGVDLIDTADSYGPFVSEQLIADALHPYGGIKIATKGSLVRYPGNSTNPSWPVIGDPAYLRQCYYMSLRRLKLEQIDLWQLHRIDPKVPRAEQFGAIREFIDEGLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="phenylacetaldehyde dehydrogenase"
/protein_id="AAF84538.1"
/db_xref="GI:9106797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6153. .7028)
/gene="XF1729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGWRGAFVSLSVVAALLLVAMAWRMPDVPGQPPERRISIGSVLGSAGVRSILFTALAW
VTAQYMLYTYIAVFAGTLGRSADVDLLLLAFGVAAIVGIWLAGVMVDRHLRLHVIGSL
VLFVAVTLVETSPASAALFAVPAMMLWGASFGGAATSIQTAASDAAGEGVDIVGAMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MNPCARPAGCGCRSRSRRALFTLTPRLSPRAWICROIARRGHGQ
AVSTITHRTPLPASSAEADTLETAALLMLAMTGFLATVTETLEAGLLPQIAQDLAIPA
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VARFLAGVSAGLSWGLLGGYARRMVVDRLKGRALAVAMVGTPLALSIGVPLGTFTGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAF84537.1"
/db_xref="GI:9106796"
/tb_xref="GI:9106796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"similar to GI|290511 (percent identity: 27 %/query alignment coverage: 84.8 %/subject alignment coverage: 84.0 %); identified by sequence similarity; putative; ORF located using Glammer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4813. .6156)
/gene="XF1728"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4813. .6156)
/gene="XF1728"
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GIELMRSRDPAVIKPVIVI"
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RLGIQFGETVLVMGLGPVGLMAVAGAALRGAGRIIGVDSRPNTVELARAYGVTDIVDF
TGGQTLEKVMALTAGQPVDSVLIASGGTASEVFTTALKAVKFGGRVACVSGFLHDESV
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ATAALPKTVGKVIGHEAVGVVEKVGENVKAFRPGDRVVLPCGNSDWRHPRAQRGEAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"similar to SP|P30864 (percent identity: 35 %/que alignment coverage: 96.6 %/subject alignment coverage: 94.1 %); identified by sequence similarity; putative; 0
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34074 bp coelicolor

cosmid

F81

BCT

23-NOV-1999

AL133171.2 GI:6468412

ABC transporter; aldo/keto reductase; dehydratase; endoglucanase; hydrolase; lipoprotein; methyltransferase; oxidoreductase; phosphatase; protease inhibitor precursor; protease precursor;

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                                                                                                                        AGACATCGGCGGTGTCGAAGAGGTTGACGCCCGAGTCCAGCGCCTCGCTCATGATCCTGA
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On Nov 26, 1999 this sequence version replaced gi:6468236.
                                                                                                                                                                                                                                                                                                                                                                                                                            sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The more significant matches with motifs in the PROSITE database also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics Dy the BBSRC and Beowulf Genomics Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)

CUSC are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary)
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Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                            Cosmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
mol. microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein kinase; tetR-family transcriptional regulator.
Streptomyces coelicolor A3(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
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                                                                                                                                                                                                                                                                                                                                                                                                       F81 Lies on the Ase-I genomic restriction fragment.
                                                                                                                                                                                                                                                  /organism="Streptomyces coelicolor A3(2)"
(strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid F8"
                                                 /note="SCF81.01,
                                                                                                                                                                                                   /gene="SCF81.01"
                                                                           /gene="SCF81.01"
                                                                                                                                                  /gene="SCF81.01"
                                                                                                                             note="nominal overlap with Streptomyces coelicolor St5B7"
                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                    identical to C-terminal region of previously sequenced
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/note="screa"
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complementing:
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/gene="SCF81.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein
/protein_id="CAB61560.1"
/db_xref="GI:6468262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCF81.02c"
/note="coro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transporter,
                    dentity in 309 aa overlap.
                                                                                                                                                                                                                           /gene="SCF81.05"
                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCF81.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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/note="SCF81
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                                                                                                                                                                                                                                                                                 .1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCF81.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .03,
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/note="SCF81.04c, possible tetr-family transcriptional regulator, len: 219 aa; similar to various Streptomyces transcriptional regulators, e.g. TR:092BKO [EMBL:ALO33161) Streptomyces coelicolor putative transcriptional regulator SC9C7.10c, 272 aa; fasta scores: opt: 189 z-score: 243.3 E(): 3.5e-06; 29.8% identity in 218 aa overlap. Contains match to Pfam entry PF000440 tetR, Bacterial regulatory
1845. .3098
/gene="SCF81.05"
/gene="SCF81.05"
/note="SCF81.05, possible serine/threonine protein kinas
/note="SCF81.05, possible serine/threonine protein kinas
len: 462 aa; low similarity to C-terminus SW:PKWA_THECU
(EMBL:U23820) Thermomonospora curvata putative
serine/threonine-protein kinase pkwA (EC 2.71.-), 742 a
fasta scores: opt: 157 z-score: 167.3 E(): 0.06; 23.68
fasta scores: opt: 157 z-score: 167.3 E(): 0.06; 23.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative tetR-family transcriptional regulator"
/protein_id="CAB61559.1"
/db_xref="GI:6468261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00440 tetR, Bacterial
regulatory proteins, tetR family, score 18.40, E-v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEAATRDHRLAATAF IGGVNGLLHDYSAGWVDATLDEVVDELVHLLLAVLRAPGPSPE
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TTVAALSEAAGLSTRQFYEEFRTLEDVLAALHLQVNAWAEEAVRTAAAGARGLPLADR
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PSRPKVLHGRDEIAEMLDDVYSRDLTHRMARCVVQGDQVAFSEECTYPDGVRVLSESM
LSLRDGEIVEQTMIQAWDE"
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/protein_id="CAB61535.2"
/db_xref="GI:6468413"
/translation="IVVMDAGRVRAVGTHRELVTADPLYAELAATQFLATGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dslavgdmpaedrarmplpsqqlnrlqdlqqlqqvtglvspvfgvvpalg
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/protein_id="CAB61535.2"
/db_xref="G1:6468414"
/translation="MISTRRIVAVVGLAAGVTGLAAPMASAAGGGPLGTEKLSVTNTL
                                                                                                                                                                                                             protein kinase,
                                                                         742 aa;
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Matches 488;
326 ccgctgagcaggccgccgtgcagcggcgaccaggcgaagacgccgagcccgtaggcctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 ccgccggaggccaccgcggggaagatctcgtccagttcggacagcgcctgctcgtccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGCGATCGGGTGCGGCGTAGGGCCGCTCCAGCTCCTCGATCTCCGTCTCGCTCAGC
                                                                                                                 acctgcgcacggccctgcgccgacttcaccgcggtgcccgcgggccagcttctccagcggt 325
                                                                                                                                                                                                        CCGCGCTCCCCGCGATGCGGGTGACGGCCTCCACCACGGCGCGGTCGCCCTCCTGGTAC
                                                                                                                                                                                                                                         ccgaggttgcggcagaacttctcgtaggcctcgatcgccggggcgcagggacggcaacagc
                                                                                                                                                                                                                                                                                                                                GGCGCGGTCACCGTGTCCTGGTGCAGCAGCCAGGGCCAGGGCCACCCGGGCGCGCGGGACG
                                                                                                                                                                                                                                                                                                                                                                    gcgccggcgatgccggggccgggacagccacccatgcgagccccacctcggccgggtcttcg
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3962. .4543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein SCF81.06c"
/protein id="CAB6157.1"
/protein id="CAB61557.1"
/db_xref="G1:6468259"
/db_xref="G1:6468259"
/translation="MRLLITSDTHLPKRAKELPAPLLAEIPRADVVLHAGDWVDTATL/translation="MRLLITSDTHLPKRAKELPAPLLAEIPRADVVLHAGDWVDTATL/translation="MRLLITSDTHLPKRAKELPAPLLAEIPRADVVHETGAAQGREARCAAR"
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/gene="SCF81.06c"
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NNWGGTADGTSVVYSRSPSADVSSDLAWREPSGYRSDHAAVSPGGTSB
LVUDMYSTPDGTSVVYSRSPSADVSSVDLATGDLNWREPSGYRSDHAAVSPGGTRA
LVDAYSTPGTSVVYSRSPSADVSSDLAVSTDAVSGYRSDHAAVSPGTRAV
VSASTSNTVHVLDIRTGEQVGSFGTGDKPHENIFTRDGRYIWNNSIGDVNTALDAPWL
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/product="putative serine/threonine protein
/protein_id="cAB61558.1"
/db_xref="GI:6468260"
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Pred. No. 2.3e-15;
0; Mismatches 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTACATCGAACTGGCCCCGATGTAGCGGACCTTGCCCGCCTTGACCAGGTCGTGCAGC 33690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGCCTGCCGGATCAGCGGACGCCAGGCCGCCTCGTCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgggcgtggtccatcaggcgcagcgcgtcgtcgtcctcgacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cccttgtagagccgccagccgtacatgtcggcggtgtcgaggcagttgatgccgcgggtcc 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTCGTCGCGGCG----GGCGAAATCGGCCAGTGCCTTGCCGACGATCTCCTCGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtgtcctcgcgccgtcgccctgggccagccagcctgcccaccagctcctcggtgtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAGTCCGGCCGTTGGGCCCGGGGCGCATCCCGGCCGTTCACCTTGGTCGCGAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGTAGTCGGTGCCCAGGCCGCAGGCTGTGGTCGATCTCGGTCATCACCGCCTTGCGG 33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacagcccgctgtcgttgacgcgctcgctcatctcgccgccgaccttggtcgccagcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atgtggtcgacgcccagcctgcgcagcgatccctcgcaggaggcgatgatgtgccgcgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccgcgaagttcgacgaggccgacgtagggaccttgccgctggcgacgaggctgtccatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACACGAACTTCGTCCAGCCGTGCCGCTCGGCGGTGTACTGCATCTTGGAGAACTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcggcggcagcacctccagctcggcgtgccggaccgccaggttgtacaggcactggtgg
                                                                                                                                                                                                                                                                  Streptomyces coelicolor
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCK13 39896 bp
Streptomyces coelicolor
AL451182
                                                                                                                                       Kinashi, H. and Hopwood, D.A.

Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
for the 8 Mb Streptomyces (1996)
                                                                                                                                                                                                                                                                                                                                                        nitrate reductase alpha chain; narH3, nitrate reductase beta chain; narH3, nitrate reductase gamma chain; narU3, nitrate reductase delta chain; oxidoreductase; peptide methionine sulfoxide reductase; regulatory protein; tetR-family transcriptional regulator; transcription elongation factor.
  Direct Submission
Submitted (11-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter ATP-binding protein; aldoketoreductase; amino acid deaminase; deaminase; dehydrogenase; DNA-binding protein; integral membrane transport protein; mark-family transcriptional regulator;
                                                                                                    Oliver, K.
                                                                                                                                                                                                                                       1 (bases 1 to 39896)
Redenbach, M., Kieser, H.M., Denapaite, D.,
                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
                                       Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane protein; metB, cystathionine gamma-synthase; narG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL451182.2 GI:13162229
                                                          (bases
                                                                                                                      (bases 1 to 39896)
                                                                                                    and
  (11-DEC-2000)
                                                            1 to 39896)
                                                                                                    Harris,D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GTACACGTTGGCGGTGTCGAAGAAGGTGACGCCGGCCTCC
Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K13
                                                                                                                                                                                                                                                                           Actinobacteridae; antomycetaceae; Streptomyces.
                                                                                                                                                                                                                                           Eichner, A., Cullum, J.,
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sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          805
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in codons is given for each CDS.

Usually the highest scoring marks found by fasta on is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK on Feb 28, 2001 this sequence version replaced gi:11691812.

Notes: Streptomyces coelicolor sequencing at The Sanger Centre is funded to the complex of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is precided by an upstream ribosome binding site sequence (optimally 5-13bb before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the BBSRC and Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strand)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(113..430)
/gene="SCK13.01c"
complement(113..430)
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/gene="SCK13.01c"
/note="SCK13.01c, hypothetical protein, len: 105 aa;
/note="SCK13.01c, hypothetical protein, len: 105 aa;
/note="SCK13.01c, hypothetical 20.2 kDa protein (fragment)
SCE6.01c, 183 aa; fasta scores; opt: 191 z-score: 22:
SCE6.01c, 183 aa; fasta scores; opt: 191 z-score: 22:
SCE6.01c, 183 aa; fasta scores; opt: 191 z-score: 22:
SCE6.01c, 183 aa; fasta scores; opt: 191 z-score: 22:
SCE6.01c, 183 aa; fasta scores; opt: 191 z-score: 22:
                              Complement(611. .1291)

/gene-"SCK13.02c"

/note-"SCK13.02c possible regulatory protein, len: 226

/note-"SCK13.02c, possible regulatory protein, len: 226

aa; similar to TR:09XXX1 (EMBL:AL357432) Streptomyces

coelicolor putative transcriptional regulator SCD95A.03c,
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"hypothetical protein"
/protein_id-"CAC18718.1"
/protein_id-"CAC18718.1"
/db_xref-"GI:11691849"
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LPGPAGVTDESGRGLALLDAPAPRWGVEQRGDRRAVRCEPAGEPPLDDVRTPAAPAVR
                                                                                                                                                                                                                                                  /gene="SCK13.02c"
complement/fil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces
/etrain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1.
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/db_xref="taxon:1902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="cosmid K13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="nominal overlap with Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .39896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1"
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gene
                                              RBS
RBS
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                                                                                                                                                                                                                                                                                            misc_feature
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                                              complement(3380. 3534. .3537
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coelicolor putative DNA-binding protein SCJ11.39c, 279 aa; fasta scores; opt: 544 z-score: 640.7 E(): 3.8e-28; 40.2% identity in 249 aa overlap. Contains Pfam match to entry PF01381 HTH_3, Helix-turn-helix and possible helix-turn-helix motif at residues 64. .85 (+4.67 SD)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1412. .2404
/gene="SCK13.03"
/note="SCK13.03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2502. .3377)
/gene="SCK13.04c"
/note="SCK13.04c, possible DNA-binding protein,
/note="SCK13.04c, possible DNA-binding protein,
aa; similar to TR:Q9R167 (EMBL:AL109949) Streptc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIREVAENSLRYLETDRIDLFYQHISDPDVPAEEVAGTVGDLITEGKVRYFGLSNVGP
RYIRRAHAVTPVTALQYEYSIFEREVEDEIIPVTELGIGLVPYELGRGFLSGVVRP
AGEYPEDDMRRWDERWGGENYAYUNAAEQLRKUATKGITPAQLALAHLAQGEDVV
PIPGTRSAARLEENVGAIDAELTEADLARIREVIPQGSAGSRYPASMMAGFRTD*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCK13.03, probable oxidoreductase, len: 330 aa; similar to TR:AAG05923 (EMBLAE004681) Pseudomonas aeruginosa probable oxidoreductase PAC35, 331 aa; fasta scores: opt: 1001 z-score: 1136.6 E(): 0; 48.2% identity 1328 aa overlap. Contains Pfam match to entry PF00248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00440 tetR, Bacterial
regulatory proteins, tetR family, score 49.20, E-v
4.1e-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2502. .3377)
/gene="SCK13.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reductase family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative oxidoreductase"
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LGVDFFDTAELYGQGTGSNETLLGNAVNDFRDEVVLATKFGFDMTSKSLGSGVNSRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mvaypgpmprspspsgqtpdaptsgggstdstrqrivaaakeefa
RHGIAGARVDRIAKQARTSKERVYAYFRSKEALYAHVAERETTALIEATQLDPADLPG
YAGILFDHFAARPDHYRLITWGRLELAESADNTSGPLQATIAGKLDKLRDAQRIGLLD
                      /note="Pfam match
Helix-turn-helix,
                                                                                                                                                                                                             AGAARGKQPVRVALLQLLDSIDTVPAYVSGRRSEILAWNRMAAALFGDWGKLPAAERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2021. .2329
/gene="SCK13.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aldo_ket_red, Aldo/keto reductase family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1400. .1404
1412. .2404
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/product="putative regulatory protein"
/protein id="CAC18717.1"
/db_xref="GI:11691848"
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                                                                                    /gene="SCK13.04c"
                                                                                                                                                         LLASWGTDAAASLPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF00248 aldo_ket_red, Aldo/keto
reductase family, score 21.20, E-value 4.9e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQRPNRLT"
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                                                                                                                                                                                   LWATHDVKEKSYGVKRMRHPLVGDLTLSFETFRLVDDDEQAFITYHAEPGSPSADALR
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, score
.3384)
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                          to entry PF01381 HTH_3, score 25.50, E-value 0.0012"
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mes 535; Conserv
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  gtgcatctggtagacgtcgatgtggtcgacgcccagcctgcgcagcgatccctcgcagga
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                                                                                                                                    GCGCTGCAGATCGGTGAGCGCGGACAGGGTCTCCTCGTCGTCGTGGCCGGGTCCCACCG
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                                                                                                                                                                     ggcgacgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcgatgtg
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3546. 4586
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/gene="SCK13.05"
/gene="SCK13.05"
/note="SCK13.05, probable dehydrogenase, len: 346 aa;
/note="SCK13.05, probable dehydrogenase, len: 346 aa;
highly similar to SW:ADH_MYCTU (EMBL.AL021287)
Mycobacterium bovis NADP-dependent alcohol dehydrogenase
AdhC, 346 aa; fasta scores: opt: 1508 z-score: 1698.9 E():
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/protein_id="CAC18714.1"
/db_xref="GI:11691845"
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Pred. No. 6.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcagttgatgccgcggtccccgggcgtggtccatcaggcgcagcgccgtcgtcgtcctcgac
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Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrene Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lin,R.M., Smith,K.A., Spencer, Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H., Hancock,R.E.W., Lory,S. and Olson,M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                     University of Washington Genome Center, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                         Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research; Institute, The First Laboratory for Plant Gene Research; 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:kaneko@kazusa.or.jp, URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-393; Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kiyakawa,C., Kohara,M., Matsumoto,M., Watsuno,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M. Takeuchi,C., Yamada,M. and Tabata,S. Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti
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Direct Submission
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Copyright (c) 1993 - 2000 Compugen Ltd.
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09xc70 streptomyce
09s0n9 streptomyce
09f825 micromonosp
09f2z5 streptomyce
09pcq4 xylella fas
09pcq5 xylella fas
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044328 agrobacteri
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09rjc4 streptomyce
09xk18 ybrio chol
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09hxb2 pseudomonas
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Matches
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                                                                                                                                                                                                                                                                                                   MEDLINE=20430101; PubMed=10972798;
Volchegursky Y., Hu Z., Katz L., McDaniel R.;
"Biosynthesis of the anti-parasitic agent megalomicin: of erythromycin to megalomicin in Saccharopolyspora ery Mol. Microbiol. 37:752-762(2000).
EMBL; AFC63245; AAG13914.1; -
SEQUENCE 330 AA; 35434 MW; 32DA7C2DDFF60997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Micromonospora megalomicea subsp. nigra.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-NRRL3275;
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Pred. No. 2.2e.
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Q9XC70
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Best Local Similarity 74.7
Matches 242; Conservative
                                                                                                       Q9SON9 PRELIMINARY;
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O1-MAY-2000 (TrEMBLrel. 13, Cr
O1-MAY-2000 (TrEMBLrel. 13, La
O1-MAY-2000 (TrEMBLrel. 13, La
DTDP-4-KETO-6-DEOXY-L-HEXOSE 2
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Q1-NOV-1999 (TrEMBLrel 12,
Q1-NOV-1999 (TrEMBLrel 12,
Q1-QT-2000 (TrEMBLrel 12,
Q1-QT-2000 (TrEMBLrel 17,
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Bacteria; Firmicutes; Act
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Pfam; PF00248; aldo_ket_red;
PRINTS; PR00069; ALDKETRDTASE
SEQUENCE 329 AA; 36144 MW
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EMBL; AF147704; AAD41
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01-OCT-2000 (TrEMBLrel. 15, Last annotation
NDP-HEXOSE 2,3-ENOYL REDUCTASE TYLCII.
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E 2,3-REDUCTASE.
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EMBL: AF563245; AAG13922.1; -. SEQUENCE 323 AA; 33511 MW; E71A81056F5BE4C7 CRC64;
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Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-MAR-2001 (TrEMBLrel. 16, Last annotation updat
TDP-4-KETO-6-DEOXYGLUCOSE 2,3 DEHYDRATASE.
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EMBL; AB032523; BAA84599.1; -. SEQUENCE 347 AA; 37775 MW; 978AD8A60B802B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=NRRL3275;
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Bacteria; Firmicutes; Actinobacteria; Ac
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. NO. 6.8e-73;
ismatches 92;
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1.4e-70;
hes 81;
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Best Local (
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Streptomyces
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Q9F2Z5;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                           Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces ocelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; AL392149; CACO8308.1; -.
SEQUENCE 330 AA; 36116 MW; 5733CFEF9F7BEEA5 CF
                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                      Redenbach M.,
Kinashi H., H
                                                                                                                                                                                                                                                                               MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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124 HIDYYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARR-HSLG :||||| || || || || || || || || || ::|
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                                                 EELVGRWLAQGGGRREDTVLATKVGGEMSER----VNDSGLSARHIIASCEGSLRRLGVD 123
                                                                                    YTQLGRTGLKVSRLVLGTMNFGPQTDESTSHDIMDAALDAGLNFVDTANVYGWGENKGRT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASAMTLDEQALSELDEIFPAVASGGAAPEAWLQ
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                                    EEIIGTWFAQGGGRRDRTVLATKVYGNMAGDGDVWPNHDKLSAVNIRRAVDASLKRLQTD 122
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                                                                                                                                            Similarity
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                                                                                                                                 Score 841; DB 2;
Pred. No. 1.7e-56;
9; Mismatches 9
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RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arruda P., Bordin S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.R.R.,
RA Colombo C., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mono E.M., Miracca E.C., Miyaki C.Y., Monteiro Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.S.S.,
RA Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.S.S.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Solva M.C.R., da Silva F.R., Silva F.R., Silva W.A.,
RA de Silva A.C.R., da Silva F.R., Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva F.R., Silva F.R., Silva W.A.,
RA da Silva A.C.R., de Suza A.M.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
"The genome sequence of the plant pathogen Xylella fastidiosa.";
RM The genome sequence of the plant pathogen Xylella fastidiosa.";
RM RA LED03946; AAFA4533 1 . .
                                                                                                                              Query Match
Best Local S
Matches 161
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                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20365717; PubMed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa
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                                                                                                                                                                                                                                                                                                                                                    AE003996; AAF84533.1;
Pro; IPR001395; -.
                                                                                                                                                           Similarity
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                      aldo_ket_red;
AA; 36339 MW
                                                                                                                                                           46.6%;
                                                                                                                                                                                                                                                                                      36339 MW;
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Pred. No. le
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                                                                                                                              Mismatches
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RESULT
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    Qy
                                                                               RA SImpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Rainach F.C., Arruda P., Baia G.S., Baptista C.S., Ra Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Ra Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Eriones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Ra Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Ra Colauto N.B., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Ra Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Ra Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Ra Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Ra Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Ra Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ra Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Ra Lemos E.G.M., Lemos M.Y.F., Lopes S.A., Lopes C.R., Machado J.A., Marcines M.V., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.M.F., Matsukuma A.Y., Mandodo M.A., Marcina E.B.L., Martins E.M.F., Matsukuma A.Y., Mandodo M.A., Marcina E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Ra Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Palmieri D.A., Paris A., Perira G.A.G., Pereira H.A. Jr., Pesquero J.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Pereira G.A.G., Santelli R.V., Sawasaki H.E., de Silva A.C.R., de Silva A.M., da Silva F.R., Silva W.A. Jr., Ra de Silva A.C.R., de Sa R.G., Santelli R.V., Sawasaki H.E., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Ra de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Ra de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Ra de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Ra de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Ra de Souza A.B., Ra de Souza A.B., Ra de Souza A.B., Ra de Souza A.B., Ra de Sou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PCQ5;
Q9PCQ5;
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDHIDLYQMHHIDRATPWEEIWQAFEQLIREGKITYVGSSNFAGWDIALAQCTAASRNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLG
                                                                   AE003996; AAF84532.1;
PF00248; aldo_ket_red; 1
NCE 362 AA; 39457 MW;
                                                 IPR001395; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma subdivision; Xanthomonas group;
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Last annotation updat
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  DD224B68B59317D0 CRC64;
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brinnell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brinnell S.C., Bron S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Enrilich S.D., Emmerson P.T.,
RA Chim S.Y., Grandi G., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kunano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Hellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
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Duesterhoeft A., Ehrlich
Submitted (APR-1997) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98044033;
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01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKALSLNLSSETLAKLDEIWP--GPGGEAPKAY
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us group; Bacillus.
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Pred. No. 1.2e-52;
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Q9KXL8;
01-OCT-2000 (TrembL)
01-OCT-2000 (TrembL)
01-OCT-2000 (TrembL)
PUTATIVE REDUCTASE.
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Tosato V., Uchiyama S.,
Viari A., Wambutt R., W
Winters P., Wipat A., Y
Yoshida K., Yoshikawa H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUNST F., OGASAWATA N., YOSHIKO SLDMITTED (NOV-1997) to the EMI EMBL; U93875; AAB80886.1; -. EMBL; 299117; CAB14626.1; -. EMBL; 29918 AA; 35475 MW;
Submitted [3]
      SEQUENCE
STRAIN=A3(2);
Cerdeno A.M., Parkhill J.,
Cerdeno ``TUN-2000) to th
                                                                       Seeger K.J
Submitted
                                                                                    STRAIN=A3(2);
Seeger K.J.,
                                                                                                                                                                         Streptomyces coelicolor.
                                                 SEQUENCE FROM N.A.
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=1902;
                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Str
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Sorokin A., Tacconi
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                                                                                                                                                                                                                                                                                                                         LNDIFP--GPGGETPEAY
                                                                                                                                                                                                                                                                                                                                                  LDEIFPAVASGGAAPEAW 331
                                                                                                                                                                                                                                                                                                                                                                         LEKFSDLCKELGEKEANVALAWVLANPVLTAPIIGPRTVEQLRDTIKAVEISLDKEILRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQRREKVVLATKVYEPISD-PNDGPNDMRGLSLYKIRRHLEGSLKRLQTDHIELYQMHHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGRREDTVLATKVGGEMSERVNDS-----GLSARHIIASCEGSLRRLGVDHIDVYQMHHI 133
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                                                                       J., Harris
(JUN-2000)
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                                                                                                                                                                                                           (TrEMBLrel. 15, (TrEMBLrel. 15, ) (TrEMBLrel. 15,
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           Barrell B.G.,
e EMBL/GenBank,
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                                                                                                                                             Streptomycetaceae;
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           Rajandream M.A
/DDBJ databases
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n Bacillus
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; Ast of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL; AL357524; CAB93413.1; -. SEDE9687B46F8435 CRC64
                                                                                                                               region genes
tumor.";
                                                                                                                                       *Kim K.S., Farrand S.K.;
"Ti plasmid-encoded genes responsible for catabolism of the crown opine mannopine by Agrobacterium tumefaciens are homologs of the region genes responsible for synthesis of this opine by the plant
                                                                                                                                                                                         STRAIN-15955
                                                                                                                                                                                                                                        Agrobacterium radiobacter.
Plasmid pTi15955.
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                Q44328
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STRAIN-A3(2);
                                                                                                                                                                               MEDLINE=96236046; PubMed=8655509;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=358;
                                                                                                                                                                                                                              Rhizobiaceae;
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                             Local
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 LGRSALLTSRLWLGTVNFSG-----RVED----DDALRLMDHARDRGINCLDTADMYGWRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIRRAVDASLKRLQTDHIDLYQFHHIDRATGFDEIWQAIDTLVQQGKVLYAGSSNFPGYK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWH 167
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                    al Similarity
122; Conser
                                                                                        PF00248;
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                     Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                               Rhizobium
                                                                     AA;
                                                                                       aldo_ket_red;
                                                                     38846 MW;
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                             28.6%;
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16,
                    46;
                   Score 495; DB
Pred. No. 4.9e
46; Mismatches
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Last annotation update)
                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 2.9e
41; Mismatches
                                                                     21D4074605E80EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                354
                   DB 2; I
1.9e-30;
nes 131;
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RESULT
Q912Z8
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Best Local Similarity
Matches 118; Conser
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01-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9I2Z8;
Q9I2Z8;
                                                                                                                                                                                                                                                                                                                                                                             Nature 406:959-964(2000).
EMBL; AE004600; AAG05128.1; -.
InterPro; IPR001395; -.
Pfam; PF00248; aldo_ket_red; 2.
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                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20437337;
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118
                                 122 VDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWH---IAAAQENAARR
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                                                                           --TGESERILGRAL-RDFAQREDLVIATKAFFPMSDRPNACGLSRKHLLASVDASLRRLG
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TDYLDLFVIHRFDPDTPIEETCETLDSLVRVGKVRYLGASSMPAWRFMKMLAFQ---
                                                                                                  LYKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLG
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                                                                                                                                                                                               HVRLGRSALLTSRLWLGTVNFSGR-----VEDDDALRLMDHARDRGINCLDTADMYGWR
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Last
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                                                                                                                                                                                                                                                            Score 472.5; DB 2
Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                         OA6E779DCDDC504C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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EMBL; AL138852; CAB72221.1; .
Interpro; IPR001395; .
Pfam; PF00248; aldo_ket_red; 2.
PRINTS; PR00069; ALDKETRDTASE.
SEQUENCE 336 AA; 37060 MW; C68A60A31C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2000)
[3]
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Submitted (FEB-2000)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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KSAQGRAQVLLPSLRPAI-EAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQL
                                              LNGWTRFVSMQDHYNLIHREAEREMLPLCADQGIGVIPWSPLARGRLTRARD---TATAR
                                                                              RRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAV
                                                                                                                                               LKRLGTDYIDLYQIHRWDYDTPIEETLEALHDVVKSGKVRYLGASSMYAWQFAKALYLAD
                                                                                                                                                                                                                                                    GYS----AGNSEEIVGQ-AVKDFARREEVVLSTKVWMRMRPGPNGAGLSRKAIFAELDAS
                                                                                                                                                                                                                                                                           MYGWRLYKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGS 116
                                                                                                                                                                                                                                                                                                                                                  YIRLGTTGLEVSAIALGCMGFGEPDRGGEPWSLGADPSRDIIR---QALEGGVNFLDTAN
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A.M., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.8%;
34.0%;
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 428.5; DB 2;
Pred. No. 5.5e-25;
8; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C68A60A31C9BB62C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic
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'DDBJ databases.
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                                                                                                                                                                                                                                                                                                                         the 8 mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

R EMBL; AL133171; CAB61562.2; -.

R InterPro; IPRO01395; -.

R InterPro; IPR001822; -.

R Pfam; PF00248; Al40_ket_red; 1.

PRINTS; PR00069; ALDKETRDTASE.

PROSITE; PS00398; RECOMBINASES_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9RJC4 PRELIMINARI,
Q9RJC4;
Q9RJC4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
01-JUN-2000 (TREMBLREL 14, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St. ACBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE ALDO/KETO REDUCTASE SCF81.28C.
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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 254
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LAWLLHQDTVTAPIVGASRPGHLEDAVAAVELTLSETEIEELE
                       LAWVLSRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELD
                                                                        FAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVG
                                                                                                 GKVRYIGASSMYAWQFSKMQYTAERHGWTKFVSMQNHYNLVYREEEREMLPLCADQGVGV
                                                                                                                         GKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGV
                                                                                                                                                    GRMRPGPNGAGLSRKAVMTEIDHSLRRLGTDYVDLYQIHRFDPHTPVEETMEALHDLVKA
                                                                                                                                                                          GEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVAS
                                                                                                                                                                                                  DEAASRPLIRQALEAGVTFFDTANVYS----DGTSEEIVGKALAD-FARRDDIVLATKVN 75
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                                                LPWSPLARGRLTRDWD-TATGRSATDTFG-STLYQEGDRAVVEAVTRIAGERGVPRARVA
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Harris D. (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOV-1999)
                                                                                                                                                                                                                                                                                                                 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hopwood D.A.;
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.;
                                                                                                                                                                                                                                                                                                                 34107 MW;
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36.0%;
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E EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                   Score 421; DB 2;
Pred. No. 1.8e-24
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                 EC2D2594595FB1B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases.
                                                                                                                                                                                                                                                                                                                 CRC64;
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296
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                                                                                                                                                                                                                                                                                                                                                                                                                                           physical map
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Best Local Similarity
Matches 116; Conserv
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STRAIN-EL TOR N16961 / SEROTYPE OI;

STRAIN-EL TOR N16961 / SEROTYPE OI;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Hackey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Ermolaeva M.D., Vamathevan J., Rass S., Qin H., Dragoi I., Sellers P.,

Erm
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Q9KU57;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRUU1393,
pfam; PF00248; aldo_ket_red; 1.
SEOUENCE 352 AA; 39549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
EMBL; AE004153; AAF93832.1; -.
TIGR; VC0667; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0XIDOREDUCTASE TAS, ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=666;
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.FVASNIIGATTMEQLKSNLDSLDISLNAELLQKIQEI 343
                                                     GIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEI 317
                                                                                                                                                                                                                                                                        FAGWHIAAAQENAARRHSIGMVSHQCLYNLAVRHAELEVLPAAQAYGIGVFAWSPLHGGL 222
                                                                                                                                                                                                                                                                                                                                                                                          LGVDHIDVYQMHHIDRSA------PWD------EVWQAMDSLVASGKVSYVGSSN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTQGKTEEFIGNWLAK-SGKREKIVLATKVAGPRNVPYIRDKMALDHRNIHQAVDDSLRR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATHVRLGRSALLTSRLWLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMY---GWR 61
                                                                                                                                                                          LSGALEKLA--AGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMQYTKLPHSSLEISKICLGTMTFGEQNSQADAFQQLDYALERGVNFIDTAEMYPVPPTA 67
                                                                                                                    LSGKYLNGARPAGARCTLHQRFSRYFTEQGILATEAYVALAQQFGLDPAQMALAFVNQRP 306
                                                                                                                                                                                                                                      ETPWGVMSYLRLAEKHELPRIVSIQNPYNLLNRSFEVGLAEISHLEGVKLLAYSPLAFGA 246
                                                                                                                                                                                                                                                                                                                                                          LQTDYIDLYQLHWPQRQTNTFGQLNYPYPDKQEEVTLIETLEALNDLVRMGKVRYIGVSN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%; Score 414.5; DB 2; 34.4%; Pred. No. 6.8e-24; tive 56; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9E37E3F477B4EA98 CRC64;
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Search completed: June Job time: 110 sec

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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	ALIGNMENTS					
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P49378 kluyveromyc	XYL1_KLULA	<u>,</u>	329	7.3	125.5	44
P78736 pachysolen	XYL1_PACTA	L	318	7.3	127	43
Q01333 erwinia her	YCR4_ERWHE	سر	103	7.5	129.5	42
P47137 saccharomyc	YJ66_YEAST	۳	282	7.7	132.5	41
P14065 saccharomyc	GCY_YEAST	ш	312	8.4	144.5	40
Q10494 schizosacch	YDG7_SCHPO	1	321	8.5	147	39
P23901 hordeum vul	ALDR_HORVU	1	320	8.6	148.5	38
P28475 malus domes	S6PD_MALDO	1	310	8.6	149	37
P14550 homo sapien	ALDX_HUMAN	ı	324	8.7	149.5	36
	MORA_PSEPU	1	295	8.7	150.5	35
P50578 sus scrofa	ALDX_PIG	<u></u>	324	8.8	152.5	34

## SEQUENCE FROM N.A. STRAIN-K12 / MG1655; MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; Mau B., Shao Y.; 01-NOV-1997 ( 15-DEC-1998 ( 15-DEC-1998 ( HYPOTHETICAL EMBL; AE000148; AAC73522.1; ALT\_INIT. EMBL; U82664; AAB40175.1; ALT\_INIT. EcoGene; EG13611; yaj0. the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W. Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. 1. SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaboration SEQUENCE FROM N.A. "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997). Escherichia coli Bacteria; Proteobacteria; Escherichia YAJO\_ECOLI P77735; between NCBI\_TaxID=562; YAJO the Swiss Institute of Bioinformatics Rel. 37, Last so (Rel. 37, Last and OXIDOREDUCTASE STANDARD; 35, 37, Created) Last sequence update) Last annotation update) UCTASE IN PGPA-ISPA INTERGENIC REGION. gamma subdivision; Enterobacteriacea PRT; 324 (See http://www.isb-sib.ch/announce/ ormatics and the EMBL outst There are no restrictions ong as its content is in À Usage ung E., Davis omp C., Kurdi Davis R.W.; bу and EMBL outstation for 0.7 commercial Υ. on ŋ

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Score 418; DB 1 Pred. No. 8e-26; 2; Mismatches 1

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YKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVND--SGLSARHIIASCEGSLRRL 120

Hypothetical protein; Oxidoreductase ACT\_SITE 127 127 HYDROGEN SEQUENCE 324 AA; 36420 MW; 0B69EC

HYDROGEN-BOND DONOR (PROBABLE).

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modified and this statement is not removed. Usage by an
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
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RESULT 3
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Q00727;
01-NOV-1997
                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              -i- FUNCTION: MAY BE INVOLVED IN THE DEHYDRATION OF 5'-
HYDROXYAVERANTIN TO FORM AVERUPIN.
-i- PATHMAY: STERIGMATCOYSTIN BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                        Brown D.W., Yu J.-H., Kelkar H.S., Fernandes M., Keller N.P., Adams T.H., Leonard T.J.;
"Twenty-five coregulated transcripts define a st cluster in Aspergillus nidulans.";
Proc. Natl. Acad. Sci. U.S.A. 93:1418-1422(1996)
                                                                                                                                                                                                                                                                                                                                                                                                             Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE STERIGMATOCYSTIN BIOSYNTHESIS (EC 1.1.1.-).
               Oxidoreductase
ACT_SITE 148
                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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15-JUL-1999
                                               EMBL; U34740; AAC49206.1;
                                                                                                                                       the European Bioinformatics Institute.
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                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaborate on the Swiss Institute of Bioinformatics and the EMBL outstation in European Hioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no
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148 H
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                 HYDROGEN-BOND DONOR (POTENTIAL,
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Query Match Best Local Similarity

18.1%; 30.2%;

Score Pred.

312; DB 1; No. 2.1e-17;

Length 387

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RESULT 4
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15-JUL-1998 (Rel. 3
AUXIN-INDUCED PROTE
                                                                                                                                                               Oxidoreductase.
ACT_SITE 136
SEQUENCE 307
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P40691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Asteridae; euasterids Solanales; Solanaceae; Nicotiana.
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Rel. 31, Last sequence update)
Rel. 36, Last sequence update)
PROTEIN PCNT115.
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                                                                         Score 307; DB
Pred. No. 3.9e
60; Mismatches
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Cheng J., Guffanti A.A., Krulwich T.A.;
Cheng J., Guffanti A.A., Krulwich T.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1995) TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                   InterPro; IPR001395; -.
Pfam; PF00248; aldo_ket_red;
                                                                                                                     SubtiList; BG11340; ycck.
                                                                                                                                                  EMBL; U30873; AAB53024.1; HSSP; P80276; 1AH3.
                                                                                                                                                                                                   EMBL; AB000617; BAA22238.1; -. EMBL; Z99105; CAB12071.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kumano M., Tamakoshi A., Yamane K.;
"A 32 kb nucleotide sequence from the region of the lincomycin-
resistance gene (22-25 degree) of the Bacillus subtilis chromos-
identification of the site of the lin-2 mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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al protein; Oxidoreductase.
127 127 HYDROGEN
310 AA; 34800 MW; C06BF4
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(Rel. 36, Last sequence update)
(Rel. 38, Last annotation update)
L OXIDOREDUCTASE IN NATB-RAPJ INTERGENIC
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HYDROGEN-BOND DONOR (PROBABLE); C06BF4195D25C91C CRC64;
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SEQUENCE
                                                                            HSSP; P2345
SubtiList;
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01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last anotation update)
15-JUL-1998 (Rel. 36, Last anotation update)
                       Oxidoreductase; Heat shock.
ACT_SITE 125 125
CONFLICT 25 25
                                                                                                                                                                                                                                            regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-I- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS,
LIMITATION AND OXYGEN LIMITATION.
-I- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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                                                                                       EMBL; Y14082; CAA74498.1; -. EMBL; Z99109; CAB12792.1; -. HSSP; P23457; 1LWI.
                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-IS58
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                Pfam;
                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                        Noback M.A.,
                                                                                                                                                                                                                                                                                                                  "First steps from a two-dimensional protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
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                                                             PF00248; aldo_ket_red;
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(JUN-1997) t
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BG13020; yhdN.
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to the EMBL/GenBank/DDBJ (
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         HYDROGEN-BOND DONOR (PROBABLE).
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RESULT 7
IOLS_BACSU
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AC P46336
CCCCCCRTTRAXX
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Best Local :
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P46336;
01-NOV-1995
                                regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-i- PATHWAY: WYO-INOSITOL CATABOLISM.
-i- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY
                                                                                                                                                                                                         STRAIN=168 / BGSC1A1;
Fujita Y., Shibayama T.,
                                                                                                                                                                                                                                                      voshida K.-I., Seki S., Fujimura M., Miwa "Cloning and sequencing of a 36-kb region genome between the gnt and iol operons."; DNA Res. 2:61-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995
30-MAY-2000
                                                                                                                                                                                 "Organization and transcription Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-168 / BGSC1
                                                                                                                                                                                                                                                                                                                                                    Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                     IOLS PROTEIN (
          This SWISS-PROT entry
                                                                                                         Antelmann H.,
                                                                                                                      MEDLINE=97443988; PubMed=9298659;
                                                                                                                                    STRAIN-IS58;
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                 "First steps from a two-dimensional
                                                                                               Hecker M.;
                                                                                                                                              SEQUENCE OF 1-20
                                                                                                                                                                      Submitted (JUN-1997)
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      MEDLINE=96093926; PubMed=7584049;
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(Rel. 32, Last sequence update)
(Rel. 39, Last annotation update)
N (VEGETATIVE PROTEIN 147) (VEG147).
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                                                                                                         Bernhardt
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J.,
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                                                                                                           Schmid
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of
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RESULT 8
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Best Local S
Matches 95
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01-FEB-1996
15-JUL-1998
"Isolation and characterization of cDNA clones for RNA species induced by substituted benzenesulfonamides in corn."; Plant Mol. Biol. 17:679-690(1991).
-1- TISSUE SPECIFICITY: LEAF AND ROOT.
-1- DEVELOPMENTAL STAGE: IT APPEARS IN ROOTS WITHIN 30 MIN OF INDUCTION, MAXIMUM LEVELS ARE REACHED BY 6 HRS, AND REMAINS CONSTANT FOR 2 DAYS. IN LEAVES IT IS SEEN 9 HRS AFTER INDUCTION AND REACHES MAXIMUM LEVELS AFTER 24 HRS.
-1- INDUCTION: BY N-(AMINOCARBONYL)-2-CHLOROBENZENESULFONAMIDE (2-
                                                                                                                                                                                                   IN2-2 OR SAF2.)

Zea mays (Maize).

Eukaryota; Viridiplantae; 1

Magnoliophyta; Liliopsida;

Andropogoneae; Zea.
                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. MISSOURI 17;
MEDLINE-92003682; PubMed-1912492;
Hershey H.P., Stoner T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
SEQUENCE
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EMBL; 299124; CAB16014.1; -.
HSSP; P23457; ILWI.
SubtiList; BG11363; iols.
Pfam; PF00248; aldo_ket_red; 1
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28.6%;
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Last sequ
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; Poales; Poaceae; PACC clade; Panicoideae
                                                                                                                                                                                                                                                                                sequence update)
annotation update)
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Pred. No. 1
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HVRLGRSA-LLTSRLWLGTVNFS---

-GRVEDDDALRLMDHARDRGINCLDTADMYG

Query Match Best Local : Matches 9

ch 16.5%; l Similarity 28.6%; 97; Conservative !

58;

Score 285; DB 1; Pred. No. 2.8e-15; 8; Mismatches 132;

Length

Indels

52;

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Oxidoreductase.
ACT_SITE 131
SEQUENCE 306 AA
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15-JUL-1999
                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
SEQUENCE
           Oxidoreductase
ACT_SITE 148
                                     EMBL; U32377; AAC49167.1;
                                                                                        modified
                                                                                                                                                                                         Appl.
                                                                                                                                                                                                           dehydrogenase gene,
                                                                                                                                                                                                                            Cary J.W., Wright M., Bhatnagar D. "Molecular characterization of an
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NRRL 3357;
MEDLINE=96156784;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                             NORA OR ADH-2.
Aspergillus flavus
                                                              or send
                                                                           entities
                                                                                                                                                                                                       cluster.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5059;
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                                                                                                                                                             1. Environ. Microbiol. 62:360-366(1996).
PATHWAY: AFLATOXIN BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHTNEVLLGK - - ALQGGVREKVELATKFGVSFADGKREIHGDPAYVRTACEGSFKRLGVD
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73; Conserv
                                                         d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                    non-profit institu
388
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             148
 AA;
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38, Last sequence update)
38, Last annotation update)
REDUCTASE (EC 1.1.1.-).
                                                                                                                                                                                                                                                        PubMed=8593042;
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33828 MW;
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43751
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HYDROGEN-BOND DONOR (POTENTIAL); 758B8187187BF5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 285;
Pred. No. 2.
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2E94674C7FDE3CBD C
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                                                                                                                                                                                                                             Aspergillus parasiticus
                                                                                                                                                                                                                                         Lee R., Chu
                                                                                                                                                                                                                 the aflatoxin
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RESULT 10
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Best Local S
Matches 97
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ACT_SITE 148
SEQUENCE 388 A
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Eukaryota; F
Eurotiales;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-ATCC 163 / NRRL 5862 / SU-;
STRAIN-ATCC 163 / NRRL 5862 / SU-;
STRAIN-ATCC 163 / NRRL 5862 / SU-;
Cary J.W., Wright M., Bhatnagar D., Lee R., Chu F.;
Molecular characterization of an Aspergillus parasiticus
Molecular characterization of an Aspergillus parasiticus
dehydrogenase gene, norA, located on the aflatoxin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q00258;
                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: AFLATOXIN BIOSYNTHESIS
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             WRLYKGHTEELVGRWLAQGGGRREDTVLATK-----VGGEMSERVNDSGLSARHIIASC
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                                          HRILSPSAGVRYSPLCLGTMSFGNGWKGVMGECDQATSFNMLDTFYESGGNFIDVANFY-
                                                                       HVRLGRSA-LLTSRLWLGTVNFS-----
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                                                                                                                                                                                                                                                                                                                                                                                                  Environ.
                                                                                                    97;
                                                                                                                Similarity
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; Trichocomaceae; mitosporic Trichocomaceae;
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38, Last sequence update)
38, Last annotation update)
REDUCTASE (EC 1.1.1.-).
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43721 MW;
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28
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Score
Pred.
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                                                                       -GRVEDDDALRLMDHARDRGINCLDTADMYG
                                                                                                                  283; DB 1
No. 4e-15;
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                                                                                                                              Length
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RESULT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AADE_YEAST
P42884;
01-NOV-1995
                                                                                                                                                                                                                   ACT_SITE SEQUENCE
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01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                SGD;
                                                                                                                                                                                                                                                                           EMBL; X83226;
EMBL; Z71607;
                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Dyck L., Pascual-Ahuir A., Goffeau A.;
Submitted (DEC-1994) to the EMBL/GenBank/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
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                                                                                                                                                                                                                                               Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                     modified
                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                              This
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                            95
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                                                                                                                 WLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQGGGR
                                                                                                                                                                                                                                                             S0005275; AAD14.
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RSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAV 194
                           RDQIVIATKFTGDYKKYEVGGGKSANYCGNHKRSLHVSVRDSLRKLQTDWIDILYIHWWD
                                                                                    WSG---FMGSMNKEQAFELLDAFYEAGGNCIDTANSY----QNEESEIWIGEWMA-SRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NA-ARRHSLGMVS-HOCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQE
                                                       REDTVLATKVGGEMSERVNDSGLSA-----RHIIASCEGSLRRLGVDHIDVYQMHHID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QGGDTERWVGEWMAQ-RQNRDEIVLSTKYTMGYTMFGPQKIKSNFQGNHAKSLRLSV 130
                                                                                                                                             86;
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                    376
                                                                                                                                             Conservative
                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                           CAA58227.1;
CAA96264.1;
                                                                                                                                                                                                                    AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32, Created)32, Last sequence update)38, Last annotation updat
                                                                                                                                                                                                                    151
41991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetaceae;
                                                                                                                                                         15.8%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       i E., Rinke M.;
the EMBL/GenBa
TO THE ALDO/KE
                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                            .' .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                           Pred.
                                                                                                                                                                                                                   HYDROGEN-BOND DONOR (POTENTIAL).; 2265406386938313 CRC64;
                                                                                                                                                                     Score
                                                                                                                                             Mismatches
                                                                                                                                                         273; DB 1;
No. 2.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD14 (EC
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                                                                                                                                             142;
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                                                                                                                                                                     Length 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                 restrictions on
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C outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRONG,
                                                                                                                                             Gaps
                                                         134
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reiser J., Muheim A., Hardegger M., Frank G., Fiechter A.;
"Aryl-alcohol dehydrogenase from the white-rot fungus Phanerochaete
chrysosporium. Gene cloning, sequence analysis, expression, and
purification of the recombinant enzyme.";
J. Biol. Chem. 269:28152-28159(1994).
-i- CATALYTIC ACTIVITY: AN AROMATIC ALCOHOL + NADP(+) = AN AROMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phanerochaete chrysosporium.
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Aphyllophorales;
Corticiaceae; Phanerochaete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corticiaceae; Ph
NCBI_TaxID=5306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
ARYL-ALCOHOL DEHYDROGENASE [NADP+] (EC 1.1.1.91) (AAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95050593; PubMed=7961751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-BKM-F-1767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L08964; AAA61931.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
  166
                                              128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
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WHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSG
                                                                                                                                                                                                                          KLGRHRQLAPGCGLHVSPIQLGAMSIGDKWHPYGMGTMDKEASFKLLDAFYNAGGNFIDT 72
                                                                                                                                                                                                                                                                    RLGR-----SALLTSRLWLGTVNFS-----GRVEDDDALRLMDHARDRGINCLDT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMSSIEEVMDSLHILVQQGKVLYLGVSDTPAWVVSAANYYATSHGKTPFSVYQGKWNVLN 214
                                         LKSMHISVHDSLRKLRTSYIDIFYVHFWDYTCTIEEVMNGLHNLVAQGKVLYLGVSDTPA
                                                                                   ARHITASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAG
                                                                                                                               ANVY----QDETSEEFIGEWM-EARGNRDQMVVATKYSLVYKRGASFEEIPQKTQYVGNS
                                                                                                                                                                           ADMYGWRLYKGHTEELVGRWLAQGGGRREDTVLATKVG------GEMSERVNDSGLS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALSIKLTPEQIEYLESIVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPEQTELEVKISEALTKIAEEHGTESVTAIAIAYVRSKAKNVFPLIGGRKIEHLKQNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPAI 254
                                                                                                                                                                                                                                                                                                             sh 15.5%;
Similarity 24.0%;
82; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydrocarbons catabolism; Oxidoreductase; NADP 153 153 HYDROGEN-BOND DONDE / DOWNE
                                                                                                                                                                                                                                                                                                                                                                                                                             385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
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                                                                                                                                                                                                                                                                                                                                                                                                                             43563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342
                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                             Score 268; DB
Pred. No. 5.9e-
73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             7D5D6E00690B9A20
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                                                                                                                                                                                                                                                                                                             DB 1; I
.9e-14;
les 147;
                                                                                                                                                                                                                                                                                                                                                          Length 385
                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                             Gaps
                                         187
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AAD4_YEAST
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Best Local S
Matches 77
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ACT_SITE 105
SEQUENCE 329
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15-JUL-1999
15-JUL-1999
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Submitted (JUL-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD4 OR YDL243C
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                                                                                                                                                                                                                                                                    117
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296 P 296
                                         319 P
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                                                                                                                                                                                                                                                                                                                                                          KFTGDYKKYEVGGGKSANYCGNHKHSLHVSVRDSLRKLQTDWIDILYVHWWDYMSSIEEV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S0002402; AAD4.
                                                                                                                                                                                                                       PAAQAYGLGVFAWSPLHGGLLSGAL---EKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                               GSMNKEQAFELLDAFYEAGGNCIDTANSY----QNEESEIWIGEWM-KSRKLRDQIVIAT 56
                                                                                     VAEEHGTESVTAIAIAYVRSKAKNVFPLVGGRKIEHLKQNIEALSIKLTPEQIEYLESII
                                                                                                                               FCRNLG-EDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEIF
                                                                                                                                                                           PMARHFGMALAPWDVMGGGRFQSKKAMEERKKNGEGLRTVSGTSKQTDKEVKIS-EALAK
                                                                                                                                                                                                                                                                    MDSLHILVQQGKVLYLGVSDTPAWVVSAANYYATSHGKTPFSIYQGKWNVLNRDFERDII 176
                                                                                                                                                                                                                                                                                                             WQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVL 202
                                                                                                                                                                                                                                                                                                                                                                                                   KVGGEMSERVNDSGLSARH-----IIASCEGSLRRLGVDHIDVYQMHH1DRSAPWDEV 142
                                       319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Conservative
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329 AA;
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36977
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Pred. No. 1.1e
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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.5; DB 1; 1.1e-13;

Indels Length

17;

Gaps

6

318

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE ARYL-ALCOHOL DEHYDROGENASE AAD4 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's-yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -Moerbe J., Schneider C., Moro M.;
mitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKFPYVFPIVGGRKVEHLYANLEALDISLSPEQMQFLNDTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEIFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces.
HYDROGEN-BOND DONOR (POTENTIAL); 62DBDD0C889610E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycotina; Saccharomycetes;
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RESULT 15
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AC P54569
DT 01-OCT
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YOKF_BACSU
P54569;
01-OCT-1996
401-OCT-1996
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Q1-FEB-1996 (Rel. 33, Created)
Q1-FEB-1996 (Rel. 33, Last sequence update)
Q1-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 37.7 KDA PROTEIN CIF7.12 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z67998; CAA91959.1; -. EMBL; Z67999; CAA91961.1; -. HSSP; P14550; ZALR.
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Hypothetical protein; Oxidoreductase.
ACT_SITE 126 126
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Eukarvota; Funqi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972;
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                                                                                                                                                ---GEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDE 316
                                                                                                                                                                                                         PLHGGLLSGALEKLAAGTAVKSAQGRAQVLLPSLRPAIEAYEK--FCRNL------
                                                                                                                                                                                                                                                                   VGSSNFAGWHIAAAQENAARRHSLGMVS-HQCLYNLAVRHAELEVLPAAQAYGLGVFAWS
                                                                                                                                                                                                                                                                                                GELSLNNEPDYTEKALDLSLKRLGIDCIDLYYVHRFSGETPIEKIMGALKKCVEAGKIRY
                                                                                                                                                                                                                                                                                                                                                          VLTHAADLGCTFWDSSDMYGF----GANEECIGRWFKQ-TGRRKEIFLATKFGYEKNPET 92
                                                                                                                                                                                                                                       IGLSECS----ANTIRRAAAVYPVSAVQVEYSPFSLEIERPEIGVMKACRENNITIVCYA
                                                                                                                                                                                                                                                                                                                            NDSGLSAR--HIIASCEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSY 157
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(Rel. 34, Created)
(Rel. 34, Last sequence
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                                              STANDARD;
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Pred. No. 4.1e-13;
""amatches 123;
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                                            PRT;
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Best Local
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Hypothetical protein; Oxidoreductase.

ACT_SITE 119 119 HYDROGEN

SEQUENCE 306 AA; 34717 MW. CTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D84432; BAA12638.1; -.
EMBL; Z99116; CAB14294.1; -.
Subtilist; BG11761; yqkf.
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the European Bioinformatics Institute.
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Submitted (MAY-1996) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168 / JH642;
Kobayashi Y., Mizuno M., Masuda
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NCBI_TaxID=1423;
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HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                           DHIDVYQMHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRH--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGL-----SARHIIASCEGSLRRLGV 122
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                                                             LKASAMTLDEQALSEL
                                                                                                                          NGYLSYSFEELTNARKAMEEVAPDL--SMTEKSLQYLLAQPAVASVITGASKIEQLRENI
                                                                                                                                                                                QGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQL-DSA
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29.7%;
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TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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Pred. No. 4.3
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB
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Perfect score:
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Match
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BLOSUM62
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## ALIGNMENTS

A;Cross-references: GB:AE003996; GB:AE003849; NID:g9106790; PIDN:AAF84533.1; GSPDB:GN A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr. J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marxino, C.L.; Marques, M.V.; Martins Chado, M.A.; Madeira, A.M.B.N.; Madeira, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.; de M.; de N.J.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.R.Ference number: A59328 밁 Š д Q В C;Accession: E82644
R;anonymous, The Xylella fastidiosa
Nature 406, 151-157, 2000 Q C; Superfamily: fission yeast pyridoxine 4-dehydrogenase C; Genetics: A; Contents: annotation A; Molecule type: DNA A; Residues: 1-329 <SIM> A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000 sugar-phosphate dehydrogenase xF1724 [imported] - xylella fastidiosa (strain 9a5c)
C; Species: xylella fastidiosa A;Status: preliminary . A; Accession: E82644 Query Match Best Local Similarity Matches 123 TDHIDLYQMHHIDRATPWEEIWQAFEQLIREGKITYVGSSNFAGWDIALAQCTAASRNLL 122 VDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSL 181 ω 8 XF1724 HVRLGRSALLTSRLWLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYK---YTHLGRTGLKVSRIALGTMNFGELTDEATSFKIMDTALDAGINFFDTADVYGGPQTPDMP KGFGTSEEYIGNWLAQDKSRRDKIVLATKVYQPMETGPNDKYLSAYHIRRACEASLKRLK 122 ---GHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLG 121 161; 46.6%; Score 804.5; DB 2; ilarity 48.8%; Pred. No. 8.2e-56; Conservative 52; Mismatches 106; Consortium of the Organization for Length 329; Indels 11.; 182 62 64 ω

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A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, H.M.B., Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.; Reference number: A59328
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A;Note: for a complete list of authors see reference number A59328 be
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D82644
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A; Residues: 1-362 <SIM>
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;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATPGLQAQIQKFRPQLEAYEALCRELGQPPAVVALAWVIHNPVVTAAISGPRTVEQMREN 329
                                                                                                                                      NFLGLVSEQSLYNLIQRTIELEVIPAVRELGIGLIPWSPIGMGLLGGVLGKITEG---RR
                                                                                                                                                                  HSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKS 238
                                                                                                                                                                                                                                                                                                                                                         DMEKGFGTSEEYIGRWLAQDKSRRDRIVLATKVYQPMGTGPNDKYLSAYHIRRACEASLK 152
                                                                                                                                                                                                                                                                                                                                                                                                           RLYKGH--TEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNYKHLGRTGLKVSRIALGCMNFGELTDEPNSFRIMSEALDSGVNLFDTADVYGGPQTP 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLQAQIDKLRPQLEAYEALCDELGQTPADVALAWLLHNPVVTAAISGPRTVEQLQQNLNA 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQG
                                                                                    AQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSA 298
                                                                                                                                                                                                                                                                                                RLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARR 178
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                                                                                                                                                                                                                                                 RLKTDHIDLYQMHHVDRSTPWQEIWQAMEQLVREGKITYVGSSNFAAWDIARAQGVAESR
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lla fastidiosa
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Pred. No. 9.6e-55;
48; Mismatches 112;
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C;Species: Agrobacterium tumefaciens
C;Date: 21-Jan-2000 #sequence_revision
C;Accession: T44934
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                                                                              mocA protein [imported] - Agrobacterium tumefaciens
                                                                                                             T44934
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, Nature 390, 249-256, 1997

Noetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardino A; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A; Liu, H; Masuda, S; Mau Y; M; Ogawa, K.; Ogiwara, A; Oudega, B; Park, S.H.; Parro, V; Pohl, T.M.; Portete Rieger, M.; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanl A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekiguchi, J; Sekowska, A; Se akeuchi, M; Tamako, T; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiya T; Winters, P; Wipat, A; Yamamoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida A; Neters, P; Wipat, A; Yamamoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida A; Reference number: A6580, MUID:98044033

Nature 300, 249-256, 1997

N; Firite, Since 300, 249-256

N; Firite, Since 300, 249-256

N; Firite, Sin
                                                                                                                                                                                 A;Gene: yrpG
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14626.1; PID:g26351A;Experimental source: strain 168
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C;Species: Bacillus subtills
C;Date: 05-Dec-1997 #sequence_revision
C;Accession: F69978
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                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain C; Genetics:
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A; Residues: 1-316 <KUN>
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Query Match
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                                  LDEIFPAVASGGAAPEAW 331
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                                                                                                                                                                                                                                                                                                                                                                                                                 SRLCLGTMNFGVDTDEKTAFRIMDEALDNGIQFFDTANIYGWGKNAGLTESIIGKWFAQG
                                                                                                                     IEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALKASAMTLDEQALSE
                                                                                                                                                                                                                                                                                        DRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQCLYNLA 193
                                                                                                                                                                                                                                                                                                                                                           GGRREDTVLATKVGGEMSERVNDS-----GLSARHIIASCEGSLRRLGVDHIDVYQMHHI 133
LNDIFP--GPGGETPEAY 314
                                                                              LEKFSDLCKELGEKEANVALAWVLANPVLTAPIIGPRTVEQLRDTIKAVEISLDKEILRM
                                                                                                                                                                                                                                                 DRRTPWDEIWEAFETQVRSGKVDYIGSSNFAGWHLVKAQAEAEKRRFMGLVTEQHKYSLL 182
                                                                                                                                                                                                                                                                                                                                 GQRREKVVLATKVYEPISD-PNDGPNDMRGLSLYKIRRHLEGSLKRLQTDHIELYQMHHI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRLWLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEELVGRWLAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 44.2%;
Similarity 50.6%;
61; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 763; DB 2;
; Pred. No. 1.4e-52;
45; Mismatches 100
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21-Jan-2000

#text\_change 21-Jul-2000

plasmid pTi15955

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probable oxidoreductase PA1739 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83427
R;Stover, C:K:; Pham, X:Q:; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, I adman, S:; Yuan, Y:, Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, I LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000.
                                                                                                                                                 A;Cross-references: GB:AE004600; GB:AE004091; NID:g9947712; A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-354 <KIM>
A; Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07785.1; PID:g797336
A; Experimental source: strain 15955
C; Genetics:
                                                                                                             A; Gene: PA1739
C; Superfamily:
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-323 <STO>
                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the plant tumor. A;Reference number: Z22872; MUID:96236046 A;Accession: T44934
                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 122; Conserv
                   Query Match 27.3
Best Local Similarity 36.3
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol.
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teriol. 178, 3275-3284, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGTAVKSAQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DGKSEEILGEIL--GGKRKGGALVATKARFNMGPGPNDGGLSRQYLIAACEASLKRLKT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNLAAADLQLSAEERKRLDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALKASAMTLDEQALSELDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVSQQIHYTLEARDAEYELLPISVDQGLGVLIWSPLAGGLLSGKHRR--NQSAPEGSRQF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGRSALLTSRLWLGTVNFSG-----RVED---DDALRLMDHARDRGINCLDTADMYGWRL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQVLLPSLRP-----AIEAYEKFCRNL EDPAEVGLAWVLSRPGIAGAVIGPRTPEQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGRSGLKVSTLTVGTMTFGGVGWAKTVGDLGVTEAKRLVDLCLDAGINLIDTADVYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGWTEPPVRDEERLWNIVDTLLSVADGRGVSAAQVALAWLIGRKAVTSIIIGGRTEAQFK
                                                                                                               fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; ilarity 38.0%; Conservative 4
                                                                                                             yeast pyridoxine 4-dehydrogenase
                                   27.3%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes
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                     57;
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Pred. No. 1.8e-31;
6; Mismatches 131
                   Score 472.5; DB 2
Pred. No. 9.5e-30;
7; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
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                                                      DB 2;
                     116;
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                                                    Length 323;
                     Indels
                                                                                                                                                                                        PIDN: AAG05128.1;
                     35;
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E85538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable NAD(P)H-dependent xylose reductase yaj0 [imported] - Escherichia coli
C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-324 <STO>
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Best Local Similarity
Matches 112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :Genetics:
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292 PEQLDSALKASAMTLDEQALSELD
                                                          237
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                                                                                                                                                                                                                           GVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVRLGRSALLTSRLWLGTVNFSGR------VEDDDALRLMDHARDRGINCLDTADMYGWR
                                                                                                                                                                                                                                                                                                    YKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVND--SGLSARHIIASCEGSLRRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDYLDLFVIHRFDPDTPIEETCETLDSLVRVGKVRYLGASSMPAWRFMKMLAFQ----RH
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                                                                                                                                                                    LGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSG-
                                                                                                                                                                                                           GMDYVDILQIHRWDYNTPIEETLEALNDVVKAGKARYIGASSMHASQFAQALELQKOHGW 176
                                                                                                                                                                                                                                                                                  -DGSSEEIVGRAL-RDFSRREDVVVATKV----FHRVGDLPEGLSRAQILRSIDDSLRRL
                                                                                                                                                                                                                                                                                                                                                          LGKTDLRVSRLCLGCMTFGEPDRGNHAWTLPEESSRPIIKRALEGGINFFDTANSYS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSLG-MYSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWH---IAAAQENAARR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TGESERILGRAL-RDFAQREDLVIATKAFFPMSDRPNACGLSRKHLLASVDASLRRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVRLGNSGLKVSRLCLGCMTYGDPAWRPWVLDEERARPFIREALEAGIDFFDSADIYS--
                                                                                            AGTAVKSAQGRAQVLLPSLRPATEAYEKFCRNLGEDPAEVGLAWVLSRPGTAGAVIGPRT
                                                                                                                                 AQFVSMQDHYNLIYREEEREMLPLCYQEGVAVIPWSPLARGRLTRPWGETTARLVSDEVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 418; DB 2; ]
Pred. No. 1.8e-25;
2; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                ---SGRVEDDDALRLMDHARDRGINCLDTADMYGWRL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
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                                                                                                                                                                      -ALEKLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                  , 116
                                                                                            291
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C; Accession: C64771

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID:97426617

A; A; Accession: C64771
                                                                                                                                                                                                     oxidoreductase Tas, aldo/keto reductase family VC0667 [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82294
                                                                                                                                                                                                                                                                                 RESULT
C82294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: fission yeast pyridoxine C;Keywords: oxidoreductase F;151/Active site: His *status predicted
A; Molecule type: DNA
A; Residues: 1-352 <HEI>
A; Cross-references: GB:
                                                                       A; Reference number: A82035; A; Accession: C82294
                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable oxidoreductase (EC 1.-.-.-) yaj0 - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                    A; Status: preliminary
                                                                                                            A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-348 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: fission yeast pyridoxine 4-dehydrogenase; Keywords: oxidoreductase
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGRSALLTSRLWLGTVNF-----SGRVEDDDALRLMDHARDRGINCLDTADMYGWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                            EEQLDELLNAVDITLKPEQIAELE
                                                                                                                                                                                                                                                                                                                                                                                               PEQLDSALKASAMTLDEQALSELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSG-----ALEKLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMDYVDILQIHRWDYNTPIEETLEALNDVVKAGKARYIGASSMHASQFAQALELQKQHGW 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVND--SGLSARHIIASCEGSLRRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGKTDLRVSRLCLGCMTFGEPDRGNHAWTLPEESSRPIIKRALEGGINFFDTANSYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEQLDELLNAVDITLKPEQIAELE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQFVSMQDHYNLIYREEEREMLPLCYQEGVAVIPWSPLARGRLTRPWGETTARLVSDEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DGSSEEIVGRAL-RDFARREDVVVATKV----FHRVGDLPEGLSRAQILRSIDDSLRRL
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GB:AE004153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.2%;
                                                                                           MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                    -AERLTGVSEELGATRAQVALAWLLSKPGIAAPIIGTSR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not shown;
GB:AE003852; NID:g9655103;
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Pred. No. 2e-25;
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 PIDN: AAF93832.1;
                                                                                                                                                                  Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burland,
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 GSPDB:GN001
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'A;Map position: 1
C;Superfamily: fission
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                                                                                       QΥ
                                                                                                                             Db
                                                                                                                                                                                                                                                                                                A; Gene: PA3795
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-316 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete genome se
A; Reference number: A82950;
A; Accession: F83170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; Lory, S.; Olson, N
Nature 406, 959-964,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                       Query Match
Best Local S
Matches 112
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Matches
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                   117
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les 116; Conser
                                                                                                                                                                                                       Local Similarity 33.9 les 112; Conservative
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LRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAA
                                                                                                                                                                  MTTDAATHVRLGRSALLTSRLWLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMYGW
                                                      RWVPGHQGGESETLIGKWLKR-TGKRDRMVIASKVGMDMGN--GHKGLSAAYIEQALERS
                                                                                         RLYKGH----TEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHITASCEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olson, M.V
                                                                                                                                                                                                                                                                                                  fission
                                                                                                                               -KLGNSGLEIPALVFGGNVFGWTADESTSFRLLDALLDAGLNCIDTADVYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000
                                                                                                                                                                                                                         23.6%;
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A; Experimental source: C; Genetics:
                                            281 GIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATHVRLGRSALLTSRLWLGTVNFSGRVEDDDALRLMDHARDRGINCLDTADMY---GWR
FVASNIIGATTMEQLKSNLDSLDISLNAELLQKIQEI
                                                                                                                                                                                               ETPWGVMSYLRLAEKHELPRIVSIQNPYNLLNRSFEVGLAEISHLEGVKLLAYSPLAFGA
                                                                                                                                                                                                                                            FAGWHIAAAQENAARRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGL 222
                                                                                                                                                                                                                                                                                                                                                     LGVDHIDVYQMHHIDRSA------PWD-----EVWQAMDSLVASGKVSYVGSSN 162
                                                                                                                                                                                                                                                                                                                                                                                                       QTQGKTEEFIGNWLAK-SGKREKIVLATKVAGPRNVPYIRDKMALDHRNIHQAVDDSLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMQYTKLPHSSLEISKICLGTMTFGEQNSQADAFQQLDYALERGVNFIDTAEMYPVPPTA 67
                                                                                                                                             LSGALEKLA - - AGTAVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRP
                                                                                                                                                                                                                                                                                                   LQTDYIDLYQLHWPQRQTNTFGQLNYPYPDKQEEVTLIETLEALNDLVRMGKVRYIGVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYKGHTEELVGRWLAQGGGRREDTVLATKVGGEMS-ERVNDS-GLSARHIIASCEGSLRR 119
                                                                                                 LSGKYLNGARPAGARCTLHQRFSRYFTEQGILATEAYVALAQQFGLDPAQMALAFVNQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 414.5; DB 2
Pred. No. 3.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                280
                                                                                                                                                                                               246
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probable oxidoreductase PA3795 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000
C;Accession: F831/0 A;Cross-references: GB:AE004798; GB:AE004091; NID:g9949963; PIDN:AAG07182.1; GSPDB:GN yeast pyridoxine 4-dehydrogenase sequence of Pseudomonas 50; MUID:20437337 Erwin, Score 408; DB Pred. No. 1.1e 52; Mismatches Coulter, A.L.; Mizoguchi, Coulter, S.N.; Fo DB 2; hi, S.D.; Folger, F aeruginosa PA01, Length 316; ; Warrener, K.R.; Kas, an opportunistic Hickey, Larbig, × × .

52;

.1e-24;

Indels

34;

Gaps

11;

60

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D84315

D84315

C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84315
C;Accession: D84315
R.Ng, W.Y; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, R.Ng, W.Y; Kennedy, S.P.; Mahairas, G.G.; Banson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab
  probable potassium channel subunit - fission yeast (Schizosaccharomyces C;Speciles: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2 C;Accession: T41659
                                                                                               RESULT
T41659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: GB:AE004437; NID:g10581102; PIDN:AAG19888.1; GSPDB:GN00138
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGSLRRLGVDHIDVYQMHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNF--AGWHIAAA 171
                                                                                                                                                                                                                                       GPRTPEQLDSALKASAMTL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TADMYG----GGRAERYIGDWLADRD--RDRYVIASKVYWPTSTAPNGRGLNRKHLRASV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADMYGWRLYKGHTEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTTDAATHVRLGRSALLTSRLWLGTVNF----SGRVE--DDDALRLMDHARDRGINCLD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGRARGEKVKGYLNERGVAILAALDEVAEQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LAAGTAVKS-AQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGA
                                                                                                                                                                                           GARTPAQLRENMAATNIEL
                                                                                                                                                                                                                                                                                                                               ---AGT-AVKSAQGRAQVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVI 287
                                                                                                                                                                                                                                                                                                                                                                               NETAARRGSEPFTVAQPRFNAVNRETVGNYLEMCREYGLGVVPWSPLAGGFLTGKYERDA
                                                                                                                                                                                                                                                                                                                                                                                                                           QENAARRHSLGMVSHQCLYNLAVRHAELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNILDRLGTDYIDILYIHRWDDATPADALMRTLDGFVREGTVHYLGASTFHPNAWKIAKA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGLDA----VPLGRTGLRVTELAFGTWRFGRETDAGDIEVGEQRAHELLDAYANAGGRFID 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIGPRTPEQLDSALKASAMTLDEQALSELD 315
                                                                                                                                                                                                                                                                                     EPPAGSRGATDQQFVDSYLTPSNFDTLDAVEAVADAVDATPAQVSLAWLRHHDQVAAPIT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R---LNLPSYQSLQPEYNLYDRADYETNLEPTVEELGIGVISYYSLASGFLSGKYRNQAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 399; DB 2;
Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NANPTQVALAWLIARPTVTAP 281
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Matches

103;

Conservative

55;

Score 384; DB 2; Pred. No. 8.2e-23; 55; Mismatches 146

146;

14;

Gaps

80

Length Indels

10

RLGRSALLTSRLWLGTVNFSGRVEDDDALRLMDHAR---DRGINCLDTADMYGWRLYKGH 66

Query Match
Best Local Similarity

22.2%;

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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                 probable potassium channel, beta subunit - Deinococcus radiodurans (strain i
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A75289
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A; Map position:
C; Superfamily: 1
                                                                                     A; Residues: 1 310 3000 A; Cross-references: GB: AE002063;
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-315 <WHI>
                                                                                                                                                                                               A; Reference number: A; Accession: A75289
                                                                                                                                                                                                                 A; Title: Genome sequence of A; Reference number: A75250;
                                                                                                                                                                                                                                                                                                                                               C; Accession: A75289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z22008
A; Accession: T41659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, May 1998
                                               A; Gene:
                                                                   C; Genetics:
                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 972h-; cosmid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 TADMYGWRLYKGHTEELVGRWLAQGGGRREDTVLATKV-GGEMSERVNDSGLSARHIIAS 112
                                               DR2317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEGSLRRLGVDHIDVYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTILGASKPEQIVENVKAVEFIDKLTPEILKKIDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNASLKRLGLPYVDVIMAHRPDPSVPMEEVVRAFTQLIQDGKAFYWGTSEWSAFEIEHAH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENAARRHSLGMVSHQCLYNLAVR-HAELEVLPAAQAYGLGVFAWSPLHGGLLSGAL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGSRLSTTFTSLAGQLQT---PEGKTQLDQVRQISKIAEQIGATPSQLALAWTLKNPYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EKLAAGTAVKSAQGRAQVLLPSLRPAIE---AYEKFCRNLGEDPAEVGLAWVLSRPGIA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
    fission
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yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                     the radioresistant bacterium MUID:20036896
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                                                                                                         GB:AE000513; NID:g6460121; PIDN:AAF11861.1; PID:g646
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Pred. No. 1.8e-23;
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                                                                                                                                                                                                                                                                                                      E.K.; Peterson,
, L.; Utterback,
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T.; Zalewski,
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April 1998 A; Description: Potassium channel beta subunit | A; Reference number: 225974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potassium channel beta subunit homolog [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-20
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <SPO>
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                                                                                                                                                                                                                                                                                                                                                                                          11 LGRSALLTSRLWLGT-VNFSGRVEDDDALRLMDHARDRGINCLDTADMYGWRLYKGHTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                        LVGRWLAQGGGRREDTVLATKV--GGEMSERVNDSGLSARHIIASCEGSLRRLGVDHIDV 127
                                                                                                                                                                                                             LYCHRPDASTPIEETVRAMNYVIDKGWAFYWGTSEWSAQQITEAWGAADRLDLVGPIVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTLDEQALSELDEIF-PA
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                                                                     ANRSLYDDYLRKYSGLKPIADELGYTLAQLAIAWCASNPNYSSYITGATRESQIQENMKA
                                                                                                                                                                           CLYNLAVRH-AELEVLPAAQAYGLGVFAWSPLHGGLLSGALEKLAAGT----AVKSAQGR 242
                                                                                                                                                                                                                                                  YQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSHQ 187
                                                                                                                                                                                                                                                                                    IMGQAIRELGWRRSDIVISTKIFWGG----PGPNDKGLSRKHIVEGTKASLKRLDMDYVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYFAHRYDPEVPMEEIVMAFDQVIRDGKALYWGTSMWPAARIAQAVEFAKANGLHAPVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYQMHHIDRSAPWDEVWQAMDSLVASGKVSYVGSSNFAGWHIAAAQENAARRHSLGMVSH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQLMGAVLRD--FPRHTLVLSSKVFWPMSDDVNDRGLSRKHVLESIDGSLRRLGTDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEELVGRWLAQGGGRREDTVLATKVGGEMSERVNDSGLSARHIIASCEGSLRRLGVDHID 126
                                                                                                      A-QVLLPSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSRPGIAGAVIGPRTPEQLDSALKA
                                                                                                                                          PEYNMFARHKVETEFLPLYTNHGIGLTTWSPLASGVLTGKYNKGAIPSDSRFALENYKNL
                                                                                                                                                                                                                                                                                                                                                           LGKSGLKVSTLSFGAWVTFGNQLDVKEAKSILQCCRDHGVNFFDNAEVYA----NGRAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVLLPSLRPATEAYEKFCRNLGEDPAEVGLAWVLSRPGTAGAVTGPRTPEQLDSALKASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPEYSMVRRDRVEQEILPYTEGAGIGLVVWSPLAMGLLTGKYDEGRPEGARLTEKENWAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   102;
VDVIPLLTPIVLDKIEQVIQSKPKRPESY
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPG20w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 18-Feb-2000
C;Accession: S61978
R;Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Sto
A;Gene: MIPS:YPL089c
A;Map position: 16L
C;Superfamily: fission
                                                                                                 A; Molecule type: DNA
A; Residues: 1-342 <WAN>
                                                                                                                                             submitted to the EMBL Data Library, A;Description: The sequence of Sacci A;Reference number: S61959 A;Accession: S61978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome see
A;Reference number: A82950;
A;Accession: B83093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable oxidoreductase PA4434 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (c;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83093 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                 C; Genetics:
                                                                                  A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDEI
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                                                                                  EMBL: U43281; NID: g1151218; PIDN: AAB68211.1;
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                                                                                                                                                                                   Saccharomyces cerevisiae chromosome XVI left
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Pred. No. 6.7e-22;
                                                                                                                                                                                                          December 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PSLRPAIEAYEKFCRNLGEDPAEVGLAWVLSR
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                                                                                  PID:g1151238;
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yeast pyridoxine 4-dehydrogenase

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281 GIAGAVIGPRTPEQLDSALKASAMTLDEQALSELDE 316
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300 --CHPIVGLNTTARVDEAIAALQVTLTEEEIKYLEE 333
                                                                                                                242 RPLNQ--STDRIKSDPTFKSLHLDNLEEEQKEIINRVEKVSKDKKVSMAMLSIAWVLHKG 299
                                                                                   225 GALEKLAAGTAVKSAQGRAQVLLPSL----RPAIEAYEKFCRNLGEDPAEVGLAWVLSRP 280
                                                                                                                                                                                                                                     65 --NGLSERIKEFLEYYSIKRETVVIMTKIYFPVDETLDLHHNFTLNEFEELDLSNQRGL 122
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Search completed: June 22, 2001, 09:25:12 Job time: 107 sec

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Minimum DB seq length: Maximum DB seq length:
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS8/gcgdat
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/SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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AAC44737
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AAT72684
AAC85191
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Streptomyces clavu
The nucleotide seq
Infected cell prot
Human adenosine Al
                                                                                                              S.erythraea erythr
Sugar biosynthesis
S. avermitilis 10
P. putida KT2440-a
                                                                                                                                                                                              Description
                                                                              Zea mays DNA fragm
Streptomyces clavu
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## ALIGNMENTS

RESULT AAX25772

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AAX25772 standard; cDNA; 3412

ВP

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WO9905283-A2.
                                          CDS
                                                                              CDS
                                                                                                                 Key
                                                                                                                                     Saccharopolyspora erythraea.
                                       /gene= "eryCIII"
/product= "desosaminyltransferase"
complement (2321..3406)
                                                                         /gene= "eryBII"
/product= "dTDP-4-keto-L-6-deoxyhexose-2,3-reductase"
complement (1045.,2310)
             /label= ORF9
/gene= "eryCII"
/product= "dTDP-4-keto-D-6-deoxyhexose-3,4-isomerase"
                                                                                                                        Location/Qualifiers
                                                                                                                complement (47..1048)
                                                                'label= ORF8
                                                                                                   label= ORF7
```

Gene cluster; bacterium; enzyme; macrolide; antibiotic; erythromycin; secondary metabolite; eryBII; eryCIII; eryCIII; hybridisation; probe; glycosylation; macrolactone; oleandomycin; ds.

S.erythraea erythromycin-synthesis gene cluster eryG-eryAIII.

08-JUN-1999

(first entry)

AAX25772;

600 589 540 529

660 649

720 709

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the eryG-eryAIII gene cluster from the Gram-positive bacterium Saccharopolyspora erythraea which encodes enzymes involved in the production of the macrolide antibiotic erythromycin as a secondary metabolite. The erythromycin gene cluster
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25-JUL-1997;
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97FR-0009458.
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No. 7.6e-144;
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e; antimicrobial; antibi
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                   96WO-US20238
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antibiotic; antifungal; fungicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 Polynucleotides (AAT72684 and AAT72685) represent 2 distinct clusters of genes encoding enzymes (AAM19734-36 and AAM19737-42) involved in sugar biosynthesis and attachment in Saccharopolyspora erythraea. The eryB genes are involved in the biosynthesis of L-mycarose and the eryC genes involved in the biosynthesis of D-desoamine. Novel glycosylation-modified polyketides are produced by selectively altering, inactivating or augmenting these eryB and/or eryC genes and introducing them into polyketide-producing
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                               ctcctgcgcggcggcgatgtgccagcccgcgaagttcgacgagccgacgtaggagacctt
                                                                                                                                                                                                                                            gaagacgccgagcccgtaggcctgcgcgggcgggcagcctccagctcggcgtgccggac
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DB; AAW19734-36.
                                                                                                CTCCTGCGCGGCGATGTGCCAGCCCGCGAAGTTCGACGAGCCGACGTAGGAGACCTT
                                                                                                                                                                             cgccgggcgcagggacggcaacagcacctgcgcacggccctgcgccgacttcaccgcggt
                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCCCCACCTCGGCCGGGTCTTCGCCGAGGTTGCGGCAGAACTTCTCGTAGGCCTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcgggggttcgcggtgacgacgccgcgcgcgatgccgggccgggacagcacccatgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttcggacagcgcctgctcgtccagggtcatcgcggacgccttcagcgcggagtcgagctg
 gatgtggtgcatctggtagacgtcgatgtggtcgacgcccagcctgcgcagcgatccctc
                                                                                                                                                              CGCCAGGTTGTACAGGCACTGGTGGGAGACCATGCCCAGGGAGTGGCGGCGGCGGCGGCGTT
                                                                                                                                                                                                                            GAAGACGCCGAGCCCGTAGGCCTGCGCGGCGGCGGCAGCACCTCCAGCTCGGCGTGCCGGAC
                                                                                                                                                                                                                                                                                         GCCCGCGGCCAGCTTCTCCAGCGCTCCGCTGAGCAGGCCGCCGTGCAGCGGCGACCAGGC
                                                                                                                                                                                                                                                                                                                                                         CGCCGGGCGCAGGGACGGCAACAGCACCTGCGCACGGCCCTGCGCCGACTTCACCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       gagccccacctcggccgggtcttcgccgaggttgcggcagaacttctcgtaggcctcgat
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                                                          /product= "Glycosyl reductase"
/gene= "AvrE"
/note= "ORF4 protein AAB61977"
complement (5709..6389)
                                                                                                                                                                                                                                                                                                   /note= "ORF2 protein AAB61974" complement (3598..4497)
                                                                                                                                                                                                                     /note= "ORF3a protein AAB61976" complement (2534..3613)
 /gene=
/note=
                                                                                                                                            /note= "ORF3b
4624..5655
                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Macrolide
/note= "ORF1 protein
                              /product= "Glycosyl
                                                                                                                                                                           /gene= "AvrC"
                                                                                                                                                                                          /product= "TDP-glucose 4, 6 dehydrase"
                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                          /gene=
                                                                                                                                                                                                                                                                         /product= "TDP-glucose synthase"
                                                                                                                                                                                                                                                                                                                                        /product= "Glycosyl.transferase'
/gene= "AvrB"
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"ORF5 protein
                                                                                                                                                                                                                                                           "AvrD"
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 AAB61978"
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AAB61973"
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Best Local Similarity
Matches 682; Conserv
                                                                                                                                                                                                                                                                                                                The invention relates to a 10 kb genomic DNA isolated from S. avermitilis that contains genes encoding proteins for glycosylation of avermectin aglycones. The polypeptides can be expressed by standard recombinant methodology. The gene and the encoded polypeptides together with other enzymatically active polypeptides, are useful to perform combinatorial blocatcalysis in vitro and in vivo in a host cell. They are useful for performing blotransformations on macrolide compounds including avermectin or other macrolide aglycones. The sequences are also useful in vivo in a bacterial host, in vitro in combination with an actionmycete
                                                                                 8784
                                                                                                                                                                                                                                                fermentation, and in vitro in combination with enzymatically active polypeptides that are not from the avermectin biosynthetic pathway to effect the synthesis of a from the avermectin active compound, e.g. an antibiotic. The present sequence represents the 10 kb genomic fragment that contain genes involved in the synthesis and/or addition of oleandrose to avermectin aglycones.
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                                                                                                                                                                                                                             Sequence
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ccccacctcggccgggtcttcgccgaggttgcggcagaacttctcgtaggcctcgatcgc
                                 ttcggtgcgcggcccgatgaccagcccggtcacgccgggccgcgacagcacccaggccat
                                             ggacagcgcctgctcgtccaggggtcatcgcggacgccttcagcgcggagtcgagctgctc
                                                                                                                        cagccaggcgtcggggggatccgccgggggaacagctcctccaggcg
                                                                                                                                    caaccaggcttccggcgccgcgccgcggaggccaccgcgggggaagatctcgtccagttc
                                                                             ggccaggacgggctcgggcagcggggtgcgcgtgcagtgccccgtccacgtgctg
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                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                              9994
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              5-16; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "ORF7 protein AA complement (8718..9761)
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complement (7858..8631)
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/gene= "AvrG"
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70.6%;
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Pred. No. 4.3e-70;
0; Mismatches 284
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                                                         microbial production
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                                                                                                     KT2440-associated
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ion strain;
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                                                       probe; amplification; vaccine
biological remediation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC (1); (3) production of expression products by culturing cells of (2); (6) expression products, or their fragments, of (1) and synthetic CC proteins or peptides with the same sequences (A); (5) poly- or CC mono-clonal antibodies (Ab) that react specifically with (A); (6) thyridoma cells that produce the monoclonal Ab of (5); (7) transgenic CC plants that contain transformed or transfected cells of (2); (8) CC detecting KT2440 using a labeled (1) or Ab as probe; and (9) DNA chips CC carrying one or more (I). (I), and their fragments, are used as probes CC to detect and isolate full-length cDNAs and/or to amplify such cDNAs by CC polymerase chain reaction, and for production of transgenic plants. (I), CC or antibodies that recognize their expression products, are used for CC detecting the presence of KT2440, particularly in presence of other, CC even closely related, bacteria. KT2440 is one of the bacteria classified as safe, by the National Institutes of Health, for genetic engineering CC and as vaccine carriers. (I) are exclusive to KT2440 with no significant CC and as vaccine carriers. (I) are exclusive to KT2440 with no significant conditions of the production of the bacteria, it chas greater catabolic activity and better survival in, and adaptation to, the rhizosphere and soil
                                                                                                                                                                                                                                                                                                                                                                   Matches 400;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel DNA sequences (I) for specific detection of Pseudomonas putida KT2440. The invention also describes (I) recombinant expression vector containing (I); (2) prokaryotic or eukaryotic cells transformed or transfected with (I) or the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TIGR-) TIGR INST GENOMIC RES.
(QUIA-) QUIAGEN GMBH.
(GBFB ) GES BIOTECHNOLOGISCHE FORWCHUNG MBH.
(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSLENTRUM.
(MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim la; Page 155; 158pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA sequences specific for Pseudomonas putida KT2440, useful safe genetic engineering host, allow detection in presence of oti
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ggcgtgccggaccgccaggttgtacaggcactggtgggagaccatgcccagggagtggcg
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                                                                  cggcgaccaggcgaagacgccgagcccgtaggcctgcggcggcggcacctccagctc
                                                                                                           ATCGGTGCGCGTGCGTTGGCCCCCGCTCCCCATGCGGTCGTCAGGCGGCCGCGCGCCAT
                                                                                                                                         caccgcg---gtgcccgcggccagcttctccagcgctccgctgagcaggccgccgtgcag
                                                                                                                                                                           CACATCGATTACCCGGCCGTCCTCCACCTCGGTCTTTTCATAGAACGACTGCCCGGATAC
                                                                                                                                                                                                    ggcctcgatcgccgggcgcagggacggcaacagcacctgcgcacggccctgcgccgactt
                                                                                                                                                                                                                                       CACCCAGGCCAGCGCAACTTGGGCCATCGGCACCCCCCGTTCGCTGGCGATNTGCTCGAC
                                                                                                                                                                                                                                                                                                      GTCCAGGTGGGCGGGCTTCGAAGCGCCGACGATAGGGGCGCTGACGCCGGCCATACCCCAG
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Pred.
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21-APR-1999

21-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                                                                                                                                                                                                                                                                                                                Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC44737 standard; DNA; 1481
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Streptomyces clavuligerus DNA sequence
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The present sequence represents DNA comprising a gene specific for 5S CC clavam biosynthesis from Streptomyces clavuligerus (SC) and which is not essential for 5R clavam biosynthesis. The present invention also CC describes: (1) a process for improving 5R clavam production in a comprise of the present invention also companies comprising manipulation of DNA as above and its inclusion in the microorganism; (2) a process for improving 5R clavam cC production in SC comprising disrupting or otherwise making defective DNA regions flanking cas 1; (3) a process for the identification of, a comprising suitable for high 5R clavam production comprising a comprosing suitable for high 5R clavam production comprising a comprising suitable for high 5R clavam production on 5S clavam cC production; (4) a microorganism which is capable of 5R clavam production and low or no 5S clavam production obtainable by a process as in (3); (5) clavulante acid (CA) obtainable by the fermentation of a comprising a clavam sin (4), and (6) CA which is free of any 5S clavam; (7) cc and the used to produce organisms capable of producing increased amounts of clavams suitably e.g. CA, for use as antiblotics. The methods can also be used to production of CA without the production of 5S clavam or clavam-2-caproxylate.
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Best Local
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5R clavum; cas1; ORF; open
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                                                                   Streptomyces clavuligerus
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                                                                                                                                                                                                         AAV50431 standard;
                                                                                           Streptomyces clavuligerus; 5R clavum; cas1; ORF; open
                                                                                                                              Streptomyces clavuligerus DNA sequence of ORFs flanking cas1.
                                                                                                                                                         26-OCT-1998
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                                                                                                        bacterial gene;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inclusion in the microorganism; (2) a process for improving 5R clavam production in SC comprising disrupting or otherwise making defective DNA regions flanking cas 1; (3) a process for the identification of a microorganism suitable for high 5R clavam production comprising a preliminary screening for microorganisms with low or no 5S clavam production; (4) a microorganism which is capable of 5R clavam production and low or no 5S clavam production obtainable by a process as in (3); (5) clavaliante acid (CA) obtainable by the fermentation of a microorganism as in (4), and (6) CA which is free of any 5S clavam; (7) CA which is free of any clavam-2-carboxylate. The methods and products can be used to produce organisms capable of producing increased amounts of clavams suitably e.g. CA, for use as antibiotics. The methods can also be used for the production of CA without the production of 5S
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Paradkar AS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of Herpes simplex virus ICP4 used in the method of the invention as modulators of apoptosis. The methods and products can be used to identify compounds which modulate (stimulate or inhibit) apoptosis in cells. They can be used to immortalise cells for the study of these cells or for growing cells in large numbers for the productions of proteins. They can also be used for stimulating apoptosis in cells, e.g. for treating a subject with a very information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0
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Pred. No. 2.2e-05;
0; Mismatches 564;
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 Query Match 8.1
Best Local Similarity 42.1
Matches 423; Conservative
                                                                                The herpes simplex virus (HSV) alpha-4 gene encodes infected cell proteinumber 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cell death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function.
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                                                              Sequence 4257
                                                                                                                                                                                                  Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                       Use of herpes simplex virus ICP4 polypeptide - useful for, blocking apoptosis in cells, production of proteins and gen
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                                                                                                                                                                                                                                                              inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense treatment of diseases and conditions. Typical diseases conditions are those associated with impaired respiration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1998;
17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114955 BP; 6071 A; 29417 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     directed against at least 2 mRNAs selected
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                                      DE19928313-A1
                                                                Streptomyces chrysomallus
                                                                                           vancomycin;
                                                                                                      N-methyltransferase
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                                                                                                                                                                                                            2043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   These compounds are often of pharmaceutical value, e.g. penicillins, vancomycin, cephalosporin, pristinamycin or actinomycin D. The modified PPS (enzymes involved in non-ribosomal peptide synthesis) are able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method of introducing an N-methyltransferase domain (A) into peptide synthetase (PPS) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Introducing N-methyltransferase activity into enzymes, useful for synthesis of N-methylated antibiotics, by altering DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-methylate their substrates but substrate specificity remains unchanged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 9; 18pp; German.
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AGTGGCCGACGGCCAGCCCCCTCGTGCTCGTGCGCGCCGCCACCGGCCCGCAGGGTGACCCGCC
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                                                                                                                                     TGTCGCCGATGAACACGGCGCCGCCGGGGGCCCAGCCGCAGCGCCCTGCTCGATGACCT
                                                                                                                                                                                                                                  ccgcggccagcttctccagcgctccgctgagcaggccgccgtgcagcggcgaccaggcga
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                               cctgcgcggcggcgatgtgccagcccgcgaagttcgacgagccgacgtaggagaccttgc
                                                                                         ccaggttgtacaggcactggtgggagagccatgcccagggagtggcggcggcgttct
                                                                                                                                                                      agacgccgagcccgtaggcctgcgcggcgggcagcacctccagctcggcgtgccggaccg
                                                                                                                                                                                                            ccgggcgcagggacggcaacagcacctgcgcacggccctgcgccgacttcaccgcggtgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81.2; Di
Pred. No. 7.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgacgcgtccgctgaagttcaccgtgccgagccagaagcctgctggtgagcagcggggaac
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                                                                                                                                                                                                                                                                                                                                                     sequence of the bleomycin
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                                                                                                                                                                                                    /note= "01
561..2309
                                                                           5806..12294
                                                                                      /transl_except=
/note= "ORF 27;
                                                                                                                                                          2767..3486
          /note= "ORF 25;
15488..21013
                                                                                                                                                                   /transl_except=
/note= "ORF 29;
                                                                                                                                                                                                                 /transl_except=
/note= "ORF 30;
                                                                                                                                                                                                                                                            ocation/Qualifiers
                               ′*tag=
                                          2291..15491
                                                     note- "ORF 26;
                                                                 /*tag=
                                                                                                              *tag=
                                                                                                                                    note= "ORF"
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                                                                                                                        ..5593
                                                                                                                                   28;
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                                                                                      (pos: 1. encodes
                                                                                                                                                                   (pos: 1. encodes
                                                                                                                                 encodes AAB07558"
                                                                                                                                                                                                                (pos: 1..3, aa: Met)
encodes AAB07556"
                     encodes AAB07561"
                                                     encodes AAB07560'
                                                                                                                                                                                                                                                                                                                                                    (BLM) gene cluster
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es AAB07559"
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es AAB07557"
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                                               99US-0115435.
99US-0118848.
2000US-0477962.
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56090..57586
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/note= "ORF 9; e
57583..58857
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/note= "ORF 23;
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/note= "ORF 15;
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'note= "ORF 10;
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note= "ORF 14;
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/note= "ORF 16;
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/note= "ORF 18;
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'note= "ORF 19;
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'note= "ORF 20;
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2893..34830
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78..49985
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                                                                                                                                     "ORF 8;
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              Chen
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                                                                                                                                    encodes AAB07578'
                                                                                                                                                              = (pos: 1..3, aa: Met)
encodes AAB07577"
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excodes AAB07572"
                                                                                                                                                                                                                                                                                                                                                                                                                                              (pos: 1. encodes
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encodes AAB07567"
                                                                                                                                                                                                (pos: 1..3, aa: Met) encodes AAB07576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pos: 1..3,
encodes AAE
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                                                                                                                                                                                                                                                           encodes AAB07574"
                                                                                                                                                                                                                                                                                                                                                 (pos: 1..3, aa: Met) encodes AAB07571"
                                                                                                                                                                                                                                                                                                                                                                                    (pos: 1..3, aa: Met) encodes AAB07570"
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              Edwards
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AAB07566"
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AAB07568"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiszolide, thiszoline, bithiszoline and bithiszoline-consaining
                                                                                                                                                                          8229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bleomycin gene cluster components useful for peptide polyketide metabolites, especially bleomycin, production chemically modifying biological molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAAB07562, AAB07563, AAB07564, AAB07565, AAB07566, AAB07567, AAB07571, AAB075721, AAB07572, AAB07573, AAB07574, AAB07576, AAB07577, AAB07578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial metabolites. The BLM gene cluster may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 97-136; 162pp; English
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hes 389;
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                                                                                                      GGCGTCGACGACGCGCGACGCTGCCGACGACGACCGTCTCGCTGGGCCCGTACTCGTTGAC
                                                                                                                        gctggcgacgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcgat
                                                                                                                                                                          GTGGACGGTGGTTGGCGATCGGCCGGCCGATGGGCACCGGGCCGGTACGGGCCGTGGC
                                                                                                                                                                                           ctgcgcggcggcgatgtgccagccgcgagattcgacgagccgacgtaggagaccttgcc
                                                                                                                                                                                                                                                                 GAGGAAGCGCTCGCCGGTGAGTTCCCGGCCGCCCCAGGTAGCCGTCGGCGACACCGGCGCC
                                                                                                                                                                                                                                                                                                                                           gacgccgagcccgtaggcctgcgcggcgggcagcacctccagctcggcgtgccggaccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTCGTGCGGGGCGCCTGGGCACCGCGGGCCGGGACCACGTAGCCGGTCAGCGTCAG
                                                                                                                                                                                                                                             GCCGATCCACAGCTCGCCGACGACGCCGTCGGGGACGGGCCGCCGCCGCTGGTCGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                CCGGCGGGCCAGGTCGCCGGTGCGGTAGACCCGGCCGTCCGGCGGGTAGTCGCTGGG
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45.3%;
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Pred. No. 8.5e-05;
0; Mismatches 452;
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67, ААВО7568,
74, ААВ<mark>О</mark>7575,
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                 DNA encoding Streptomyces ambofaciens platenolide synthase domain for production of spiramycin-related polyketide antibiotics
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P-PSDB; AAW23716-W23720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44377 BP; 4965 A; 15552 C; 17381 G; 6479
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catctcgccgccgaccttggtcgccagcacggtgtcctcgcgccgtccgccgccctgggc 774
                                                                 gaccttgccgctggcgacgaggctgtccatggcctgccacacctcgtcccacggcgcgga
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                                         GGCCGGGGGCCGGAGTCGGCCGGGTTCCGCAGGACCCGGCGGCCGAAGACGCCCGC---
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44.78;
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Pred. No. 0.00018;
0; Mismatches 537;
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RESULT 15
AAT80414/C
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                                                                                                  production
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                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene is the tylactone synthase gene cluster of the invention. The tyld sequence was isolated from Streptomyces fradiae, and encodes multifunctional proteins which direct the synthesis of the polyketide tylactone. Tylactone is the basic building block of the antibiotic tylosin. The hybrid sequence can be used to transform S. ambofaciens lacking the srmG ORF1 sequence, or S. fradiae lacking the tylG ORF1 sequence, so that they can produce polyketides. The DNA sequence can be sequence, so that they can produce polyketides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified so as to alter the type of carboxylic acids incorporated, t number of carboxylic acids incorporated and/or the post-condensation reactions performed, thereby resulting in novel tylosin-related
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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## ALIGNMENTS

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576.
FILLING DATE: 21-DEC-1995
                 SEQUENCE CHARACTERISTICS:
LENGTH: 3756 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                               REGISTRATION NUMBER: P-40,9
REFERENCE/DOCKET NUMBER: 58
TELECOMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Dianne Casuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
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STREET: 100 Abbott
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
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RESULT 2 US-08-690-473-1/c

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; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-690-473-1
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FILING DATE: 26-JUL-1996
CLASSIEICATION: 435
ATTORNEY/AGENT INFORMATION: 435
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37.642
REFERENCE/DOCKET NUMBER: ARCD:239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Leopardi,
APPLICANT: Roizman,
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LENGTH: 4257 base pair
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MEDIUM TYPE: Floppy
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ZIP: 77210
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gtacaggcactggtgggagaccatgcccagggagtggcggcggcggcggttctcctgcgc 489
                                                           GGGGCCCGCGGGTCCCTCCGGCCGCGGGGGCTGGCCGGGCCCGGGCCCCGGCCAGCCCCGG
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Pred. No. 1.3e-07;
0; Mismatches 564;
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SEQ ID NO 1
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                                                                                                                                                                               -09-259-821A-1
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/259,821A CURRENT FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/690,473 PRIOR FILING DATE: 1996-07-26 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                            LENGTH: 4257
TYPE: DNA
ORGANISM: HERPES
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42.9%;
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                                                                                                          Score 84.6; DB 4;
Pred. No. 1.3e-07;
0; Mismatches 564;
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; Sequence 1, Application US/08843659
Patent NO. 6218103
; GENERAL INFORMATION:
APPLICANT: Leopardi, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLE
TITLE OF INVENTION: INHIBITORS OF
NUMBER OF SEQUENCES: 6
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CORRESPONDENCE ADDRESS:

Bernard
HERPES SIMPLEX VIRUS US3
INHIBITORS OF APOPTOSIS
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AND ICP4 AS

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US-08-843-659-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
                                                                      2130 GACGGCCGCCAGGTCGCCGTCGAAGCCCTCGGCCAGCGCCTCCAGGATCCCGCGGCAGGC 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2310 GCCGGCCACGCGCAGGTCCCCGCGCAGGCGCATGAGCACCAGCGCGTCGCGCACGAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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550 gacgaggctgtccatggcctgccacacctcgtcccacggcgcggaccggtcgatgtggtg 609
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 cgcctgctcgtccagggtcatcgcggacgccttcagcgcggagtcgagctgctcgggggt 129
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/843,659
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(512) 474-7577
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Pred No. 1.3e-07;
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; Sequence 7, Application US/08804227C

; Patent No. 5876991
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                           STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
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                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1530
                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCI(DOS) TE CURRENT APPLICATION DATA:
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                                                                                                                      SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
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CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON OPERATING SYSTEM: SOFTWARE: ASCI(DO
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Rosteck, Paul R., Jr.
Sutton, Kimberly L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                  February 21,
N: 435
                                                                single
                               (genomic)
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Best Local Similarity 44.7
Matches 448; Conservative
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                                 CATCCGTACGGCGATCTGGTCCTCGCCGCCGGGTTCGGCGAGGACGCCGGCGAGACGGTC
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Pred. No. 2.2e-
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2.2e-06;
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                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                              LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3885
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                                                                            FEATURE:
NAME/KEY:
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OPERATING SYSTEM:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PAUL R. CANTRELL 1138 STREET: LILLY CORPORATE CENTER
                                                                                                           LOCATION:
                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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nucleic acid
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Kuhstoss, Stuart
Rao, Nagaraja R.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Matches 424;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (215) 568-343
INFORMATION FOR SEQ ID NO:
                                                                                                                                            4244
 4364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DF TELECOMMUNICATION INFORMATION:
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NAME: Leary Ph.D., Kathryn I
REGISTRATION NUMBER: 36,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Composition TITLE OF INVENTION: Infections
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                                                                                                                                                                                                                                      10 ggcttccggcgccgcgccgcggaggccaccgcgggggaagatctcgtccagttcggacag 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/065,146 FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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GCCGGCCACGCAGGTCCCCGCGCAGGCGCATGAGCACCAGCGCGTCGCGCACGAACCG
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                                                                                                                                                                                                                   GGCGTCCGGTGCGCTGGCCGCCGCCAGCAGCAGGGGCGCAGGCTCTGGTTGTCAAACAG
                            ctcggccgggtcttcgccgaggttgcggcagaacttctcgtaggcctcgatcgccgggcg 249
                                                                   GCCCAGGGCCCCGGCGACCAGGCTCACGGCGCGCACGGCGACGGCCACGGCCTCGCTGCC
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One Liberty Place, 46th floor
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Pred. No. 4.9e-06;
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                                                                                                             GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: ROSteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNINUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                  Sequence 1, Application US/08804227C Patent No. 5876991
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                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 15
STREET: LILLY CORPORATE CENTER
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COMPUTER READABLE FORM:
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                                                      CITY: INDIANAPOLIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 371;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            41116
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                                                                                                                                                                                                                                                                                                                                                                                                                                           41236
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                                                                                                               40936
                                                                                                                                                                               40996
                                                                                                                                                                                                                                             41056
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LENGTH: 43280 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           95
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SOFTWARE: ASCI(DOS)
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aggccgccgtgcagcggcgaccaggcgaagacgccgagccgtaggcctgcgcggcgggc
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                                                GCGGCACCGGTCCCGGGGCCGCCGGGTCCGTGGTCCCGTGCGGTGGCGAGCAGTTCGGCC
                                                                                                              GTCCCGAAGGCGGGGCGGAACCGGGGAAGCGGCGGCGAGCAGTTCCGGCGATTTCCGCGGGCC
                                                                                                                                                                                              cggccctgcgccgacttcaccgcggttgcccgcggccagcttctccagcgctccgctgagc 334
                                                                                                                                                                                                                                           AGCCCGGTGTCCTCCGCGCGTCGGCCAGCGGCACGAGGGCCACCGGCTGCCGGTCCGCC 40997
                                                                                                                                                                                                                                                             cggcagaacttctcgtaggcctcgatcgccgggcgcagggacggcaacagcacctgcgca 274
                                                                                                                                                                                                                                                                                                                                   atgccgggccgggacagcacccatgcgagcccacctcggccgggtcttcgccgaggttg
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                                                                            agcacctccagctcggcgtgccggaccgccaggttgtacaggcactggtgggagaccatg
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20010..31199
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US-08-042-747A-7/c
; Sequence 7, Application US/08042747A
; Patent No. 5487969
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                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scinicariello, Franco
APPLICANT: Hilliard, Julia K.
TITLE OF INVENTION: Cloning and Amplification
TITLE OF INVENTION: Virus Genes
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APPLICANT:
                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 3518
                                                                                                                         REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
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                      TYPE: nucleic acid
             STRANDEDNESS:
                                                                                              TELEX:
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TOPOLOGY:
                                                                                                           TELEFAX:
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                                                                                                          210-226-8395
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Scinicariello, Franco
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RESULT 10
5212296-8/C
;Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER,
; J.; O'KEEFE, DANIEL P.;OMER, CHARLES I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
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US-08-042-747A-7
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Pred. No. 2.5e-05;
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Best Local Similarity 47.5
Matches 384; Conservative
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FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION UNMBER: 405,605
FILING DATE: 11-SEP-1989
2 ID NO:8:
                                                                                                                                                                                                                                                                                           1143
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                                                                                              cgccgccgaccttggtcgccaggcacggtgtcctcgcgccgtccgccgccctgggccagcc 779
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ACAGGCGTCCCATGGTGGCGATCTGGGTGTCGTCGAGCTCGCCGGGGCGACCAGGCGGC
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Pred. No. 3.2e-05;
0; Mismatches 403;
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                                                                  Query Match
Best Local Sir
Matches 305;
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                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/FF
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92,
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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 3347
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ORGANISM: S.p.
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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TCGGCCGGCCCGGCCAGCGCAGCAGGAGGATCTTGGCGTGCCGGTGCCTGCTTCACC 3288
                                                                  Similarity 45.4
05; Conservative
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1300 I Street, N.W., Suite 700
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Zagorec, Monique
Debussche, Laurent
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                                                                Score 71.2; DB 2;
Pred. No. 3.2e-05;
0; Mismatches 358;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TITLE OF INVENTION:
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                                                                                                                                                             NUMBER OF SEQUENCES:
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                                              COUNTRY: USA
ZIP: 20005-3315
                                                                                    STATE:
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                                                                                                              E: Finnegan, Henderson, 1300 I Street, N.W., Su
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                                                                                                                                                                                                                                                                                                      Jacques,
                                                                                                                                                                                                                                                                                                                     Crouzet,
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                                                                                                                                                                                                                                         Debussche, Laurent
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Joel
                                                                                                                                                                 Polypeptides Involved In The Biosynthesis Of Streptogramins, Nucleotide Sequences
                                                                                                                                                                                                                                                                                        Nathalie
Patricia
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Best Local Similarity
Matches 305; Conserv
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 10-MAY-1995 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                  2987
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ANTI-SENSE: NO
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                                        2927 GCCTGGTCGGCCGGGAGCGGGGGGGGTGATCAGGCCGATGTGCTCGGTGACGGCGGCCAGC
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   707
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FILING DATE: 25-SEP-1993
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cgctcgctcatctcgccgccgaccttggtcgccagcacggtgtcctcgcgccgtccgccg
                                                                         cgcagcgatccctcgcaggaggcgatgatgtgccgccgccgacagcccgctgtcgttgacg
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PatentIn Release #1.0, Version
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                                                                                                           TELEFAX: (202) 408-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Debussche APPLICANT: De Crecy-TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                              REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                           FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 25-SEP-1992
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                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                         MOLECULE TYPE:
                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                        TYPE: nucleion STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 10-MAY
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                            TOPOLOGY:
                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/FR 93/00923
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins,
VENTION: Coding For These Polypeptides A
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Zagorec, Monique
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Lacroix, Patricia
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Blanche, Francis
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And Their Use
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; ORGANISM: S.p
US-09-231-818-1
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Best Local Similarity
Matches 305; Conserv
                                                                                                                                                                      Patent No. 5589385
                                                                                                                                                         GENERAL INFORMATION:
                                          APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation
TITLE OF INVENTION: useful therein
                CORRESPONDENCE
                                                                                                                        APPLICANT:
APPLICANT:
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                                NUMBER OF SEQUENCES:
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                                                                                                                      Ryan, Michael J.
Lotvin, Jason A.
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American Cyanamid Company
                ADDRESS
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Best Local :
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                            427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Tsevdos, Estelle J
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TYPE: n
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/125,468 FILING DATE: 22-SEP-1993
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                                                                                                                                      CCCGCGCTCGGCGGCCCGTCCGGGGTCTCCAGCACGAGCAGTGCGCCGCCCCTCGCCCGG
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ilarity 45.1%;
Conservative
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Pred No. 3.5e-
0; Mismatches
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tches 420;
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US-08-474-933-1
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                                                                                         US-08-474-933-1
Query Match 7.1%;
Best Local Similarity 45.1%;
Matches 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                       TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24069 G 24069
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                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cloning of the biosynthetic pathway for TITLE OF INVENTION: chlortetracycline and tetracyline Forma
                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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Fantini, Susan E.
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Lotvin, Jason A.
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ne Cyanamid Plaza
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                                                                                                       DNA (genomic)
                                                                                                                                       single
                   7.18;
45.18;
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   Score 71; DB Pred. No. 3.56 0; Mismatches
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                                      DB 2;
                                      Length 30001;
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